Paul Schulwitz

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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 6-17-05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 09/915,814
Location (Bldg/Room#): 2D28 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK
****

mej

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: AS Mod to H S L Exp.

Inventors (please provide full names): Butler et al.

Earliest Priority Date: 7/26/01

Search Topic:
Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only *Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Please search Seq ID No: 3

- Between NTS 1 — 970 only.
- Score over length
- 70% homology limit
- Size range 8 — 50 NTS.

No interference Please.

Thanks.

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Type of Search

_____ NA Sequence (#)
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_____ Structure (#)
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_____ Litigation
_____ Fulltext
_____ Other

Vendors and cost where applicable

_____ STN _____ Dialog
_____ Questel/Orbit _____ Lexis/Nexis
_____ Westlaw _____ WWW/Internet

____ In-house sequence systems

____ Commercial ____ Oligomer ____ Score/Length
____ Interference ____ SPDI ____ Encode/Transl
_____ Other (specify)

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 27, 2005, 16:56:58 ; Search time 8 Seconds
(without alignments)
3.735 Million cell updates/sec

Title: us-09-915-814-3
Perfect score: 970
Sequence: 1 cttcttgtaagagagtgcta.....tttctgagtgggtcgcagat 970

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 830 seqs, 15403 residues

Total number of hits satisfying chosen parameters: 1660

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 838 summaries

Database : rngdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	22	2.3	31	1	AAI29665	Human single nucle
c	2	21.6	2.2	29	1	AAA04056	Polymorphic fragme
c	3	20	2.1	20	1	ABZ82630	Human HSL chimeric
c	4	20	2.1	20	1	ABZ82640	Human HSL chimeric
c	5	20	2.1	20	1	ABZ82631	Human HSL chimeric
c	6	20	2.1	20	1	ABZ82643	Human HSL chimeric
c	7	20	2.1	20	1	ABZ82633	Human HSL chimeric
c	8	20	2.1	20	1	ABZ82638	Human HSL chimeric
c	9	20	2.1	20	1	ABZ82635	Human HSL chimeric
c	10	20	2.1	20	1	ABZ82637	Human HSL chimeric
c	11	20	2.1	20	1	ABZ82639	Human HSL chimeric
c	12	20	2.1	20	1	ABZ82634	Human HSL chimeric
c	13	20	2.1	20	1	ABZ82632	Human HSL chimeric
c	14	20	2.1	20	1	ABZ82636	Human HSL chimeric
c	15	20	2.1	20	1	ABZ82641	Human HSL chimeric
c	16	20	2.1	20	1	ABZ82642	Human HSL chimeric
c	17	18.8	1.9	26	1	ADD01367	Human TCH099 codin
c	18	18.6	1.9	25	1	ACK19838	Human microarray D
c	19	18.4	1.9	24	1	AAD57923	M. tuberculosis Rv
c	20	18.2	1.9	24	1	AAT94895	Human G protein co
	21	18.2	1.9	25	1	ABN12495	Human GDMLP-1 25-m
	22	18.2	1.9	25	1	ABN12493	Human GDMLP-1 25-m
	23	18.2	1.9	25	1	ABN12494	Human GDMLP-1 25-m
	24	18.2	1.9	25	1	ACN75585	Human GDMLP-1 prob
	25	18.2	1.9	25	1	ACN75584	Human GDMLP-1 prob
	26	18.2	1.9	25	1	ACN75583	Human GDMLP-1 prob
c	27	17.8	1.8	25	1	ACK19737	Human microarray D
	28	17.6	1.8	25	1	ACH58053	DNA target sequenc
c	29	17.4	1.8	20	1	AAT11438	Retinoblastoma gen
	30	17	1.8	20	1	AAZ69909	Human biallelic ma
c	31	16.8	1.7	20	1	AAA96514	Primer used to amp
c	32	16.8	1.7	20	1	ADI79687	Mouse HMG-CoA redu
	33	16.8	1.7	20	1	ADI79880	Mouse HMG-CoA redu
	34	16.8	1.7	21	1	ACC70796	Human Toll-like re
c	35	16.8	1.7	22	1	AAF60216	Human ATM gene exo
c	36	16.6	1.7	23	1	ADG29459	CCND1 siNA-target
c	37	16.6	1.7	23	1	ADN34460	Cyclin D1 transcri
c	38	16.4	1.7	21	1	ADH93721	Human gene PCR pri
c	39	16.4	1.7	21	1	ADR32217	Human Pdx-1 forwar
	40	16.2	1.7	21	1	ADB17808	Wheat starch synth
	41	16.2	1.7	21	1	ADM29499	Human novel protei
	42	16.2	1.7	22	1	AAA96184	Primer for a type
	43	16.2	1.7	22	1	AAH91298	Human inflammatory
	44	16.2	1.7	22	1	AAD49629	Human EPO gene spe
c	45	16.2	1.7	23	1	AAH56004	Human SCN2A PCR-SS
c	46	16	1.6	20	1	ABZ92750	Human oligonucleot
c	47	16	1.6	20	1	ABD28980	N58473-derived oli
c	48	15.8	1.6	19	1	ADF84128	Human breakpoint c
	49	15.8	1.6	19	1	ADF83865	Human breakpoint c
c	50	15.8	1.6	20	1	AAQ85691	Intronic primer fo
	51	15.8	1.6	20	1	AAT89333	RSV F gene (nucleo
c	52	15.8	1.6	20	1	ADN31411	Human forkhead box
	53	15.8	1.6	20	1	ADN31529	Human forkhead box
c	54	15.8	1.6	21	1	ADK96735	Primer of the inve
	55	15.6	1.6	22	1	ADI33144	PCR primer 1 used
	56	15.6	1.6	22	1	ADQ76782	Human LGR6 splice
	57	15.4	1.6	17	1	ABN07601	Human GDMLP-1 17-m
	58	15.4	1.6	17	1	ABN07600	Human GDMLP-1 17-m
c	59	15.4	1.6	17	1	ABV91103	Human POSHL1 scann
c	60	15.4	1.6	17	1	ABV91101	Human POSHL1 scann
	61	15.4	1.6	17	1	ADI48562	Human tumour suppr
	62	15.4	1.6	17	1	ACC52241	Human tumour suppr
	63	15.4	1.6	17	1	ACN70690	Human GDMLP-1 prob
	64	15.4	1.6	17	1	ACN70691	Human GDMLP-1 prob
c	65	15.4	1.6	20	1	AAC83280	PCR primer used sp
	66	15.4	1.6	20	1	ADD56698	Human gene express
	67	15.4	1.6	20	1	ADH94177	Human gene PCR pri
c	68	15.4	1.6	20	1	ADH50650	Human IRAK-1 DNA,
	69	15.4	1.6	20	1	ADN30060	Human cytokine-ind
	70	15.4	1.6	20	1	ADP71229	Rat glutamate rece
	71	15.4	1.6	22	1	ABX72480	Human NOVX DNA PCR
c	72	15.2	1.6	20	1	AAZ04798	PCR primer used to
	73	15.2	1.6	20	1	AAA11885	Human MDMX antisen
c	74	15.2	1.6	20	1	AAA66201	Dog genomic marker
c	75	15.2	1.6	20	1	ADK76020	Chimeric phosphoro
c	76	15.2	1.6	20	1	ADK75958	Chimeric phosphoro
c	77	15.2	1.6	20	1	ADJ10297	Phosphorothioate a
	78	15.2	1.6	20	1	ADJ10365	Target DNA oligo f
	79	15.2	1.6	20	1	ADM14353	Human mPGES-1 chim
	80	15.2	1.6	20	1	ADN31530	Human forkhead box
c	81	15.2	1.6	20	1	ADN31412	Human forkhead box
c	82	15.2	1.6	20	1	ADP77448	Chimeric phosphoro
c	83	15.2	1.6	20	1	ADP77832	Chimeric phosphoro
c	84	15.2	1.6	20	1	ADP77215	Chimeric phosphoro
c	85	15.2	1.6	20	1	ADQ09501	Murine Angiopoieti
	86	15.2	1.6	20	1	ADQ09573	Murine Angiopoieti
c	87	15.2	1.6	20	1	ADP83556	Human mtDNA specif
c	88	15.2	1.6	20	1	ADP68653	Human PPAR-alpha a
c	89	15.2	1.6	20	1	ADK22528	Acyl-coenzyme A sy
c	90	15.2	1.6	20	1	ADR72435	Antisense oligo ta
	91	15.2	1.6	21	1	AAQ84606	D-loop mtDNA prime
c	92	15.2	1.6	21	1	AAT34674	Human cytochrome P
c	93	15.2	1.6	21	1	AAX15019	Sense PCR primer u
c	94	15.2	1.6	21	1	AAC64753	Secreted protein N
c	95	15.2	1.6	21	1	AAL51986	FGFR RT-PCR primer
c	96	15.2	1.6	21	1	ACA06021	Human CXC type che
	97	15.2	1.6	21	1	ACA99378	Recombinant anti-I
c	98	15.2	1.6	21	1	ACD13612	Human IL-8 DNA PCR
c	99	15.2	1.6	21	1	ADO30680	Interleukin-8 gene
c	100	15	1.5	17	1	ABV91102	Human POSHL1 scann
	101	15	1.5	18	1	AAV33862	Primer FTC-9 for r
	102	15	1.5	18	1	AAX75966	SB transposase PCR
	103	15	1.5	18	1	ADD41947	Transposon vector
	104	15	1.5	21	1	AAF97288	Human gene single
c	105	14.8	1.5	18	1	AAZ30583	Human integrin alp
	106	14.8	1.5	18	1	AAH62926	Shrimp white spot

c 107	14.8	1.5	18	1	AAS10245	Antisense oligonuc
c 108	14.8	1.5	18	1	AAD20374	Antisense oligo, I
c 109	14.8	1.5	18	1	AAD41925	Human SRC-1 antise
110	14.8	1.5	18	1	AAD51440	hGH-V gene fragmen
111	14.8	1.5	18	1	ADR44784	Human hC6 sense ol
c 112	14.8	1.5	18	1	ADR44782	Human hC6 antisens
113	14.8	1.5	19	1	AAV08207	PCR primer ABCR.EX
c 114	14.8	1.5	19	1	AAD51441	hGH-V gene fragmen
115	14.8	1.5	19	1	ABX13143	Rat p11 mutagenic
c 116	14.8	1.5	19	1	ADO18775	Analytical probe c
c 117	14.8	1.5	19	1	ADO18369	Analytical probe c
c 118	14.8	1.5	19	1	ADO18575	Analytical probe c
c 119	14.8	1.5	19	1	ADO18248	Analytical probe c
c 120	14.8	1.5	19	1	ADT01909	Novel mutant prote
121	14.8	1.5	20	1	AAQ39534	PCR Primer #2 for
122	14.8	1.5	20	1	AAQ82614	Chromosome 11 (loc
123	14.8	1.5	20	1	AAT15114	Hypermutable targe
c 124	14.8	1.5	20	1	AAT15134	Hypermutable targe
125	14.8	1.5	20	1	AAV21006	Microsatellite DNA
c 126	14.8	1.5	20	1	AAV21038	Microsatellite DNA
c 127	14.8	1.5	20	1	AAV18196	Primer for Fanconi
c 128	14.8	1.5	20	1	AAZ21694	Exemplary oligonuc
129	14.8	1.5	20	1	AAZ21662	Exemplary target n
130	14.8	1.5	20	1	AAZ01970	PCR primer used to
131	14.8	1.5	20	1	AAZ05591	PCR primer used to
c 132	14.8	1.5	20	1	AAA09682	Human SHP-1 antise
133	14.8	1.5	20	1	AAC73703	Human IL-5 antisen
134	14.8	1.5	20	1	AAF85110	PCR primer for cDN
135	14.8	1.5	20	1	AAL40329	Human caspase 6 an
136	14.8	1.5	20	1	AAD27828	Primer A used in P
c 137	14.8	1.5	20	1	ABS68900	Human RecQ protein
138	14.8	1.5	20	1	ABX04357	Human Interleukin
139	14.8	1.5	20	1	ADC65775	Human TGF-beta rec
140	14.8	1.5	20	1	ADC10441	Human NOVX polypep
c 141	14.8	1.5	20	1	AAD62218	Human haematopoiet
c 142	14.8	1.5	20	1	ABZ99357	Human PDE4C oligon
143	14.8	1.5	20	1	ABZ85975	Human oligonucleot
144	14.8	1.5	20	1	ABZ91021	Human oligonucleot
145	14.8	1.5	20	1	ACC83590	Human Toll-like re
c 146	14.8	1.5	20	1	ABD32388	Human PDE4C-derive
147	14.8	1.5	20	1	ABD22205	Human stanniocalci
148	14.8	1.5	20	1	ABD27251	AA180912-derived o
149	14.8	1.5	20	1	ADK95099	Primer of the inve
c 150	14.8	1.5	20	1	ADJ61242	Oligonucleotide as
c 151	14.8	1.5	20	1	ADO46632	Human oligonucleot
152	14.8	1.5	20	1	ADO52426	Human BRCA2 region
c 153	14.8	1.5	20	1	ADO52460	Human BRCA2 region
c 154	14.8	1.5	20	1	ADP22034	Ornithine decarbox
155	14.8	1.5	20	1	ADP21936	Ornithine decarbox
c 156	14.8	1.5	20	1	ADP83554	Human mtDNA specif
c 157	14.8	1.5	20	1	ADP83555	Human mtDNA specif
c 158	14.8	1.5	20	1	ADP83557	Human mtDNA specif
159	14.8	1.5	20	1	ADR12034	Human interleukin-
c 160	14.8	1.5	20	1	ADT00344	Novel mutant prote
c 161	14.8	1.5	21	1	ADQ26790	Beta-catenin oligo
162	14.6	1.5	15	1	ABK95939	Human LIPE gene po
c 163	14.6	1.5	15	1	ABK95975	Human LIPE gene po
164	14.6	1.5	15	1	ABK95968	Human LIPE gene po
c 165	14.6	1.5	15	1	ABK95969	Human LIPE gene po
166	14.6	1.5	15	1	ABK95974	Human LIPE gene po
167	14.6	1.5	15	1	ABK95941	Human LIPE gene po
c 168	14.6	1.5	15	1	ABK95971	Human LIPE gene po
169	14.6	1.5	15	1	ABK95972	Human LIPE gene po
170	14.6	1.5	15	1	ABK95970	Human LIPE gene po
171	14.6	1.5	15	1	ABK95978	Human LIPE gene po
172	14.6	1.5	15	1	ABK95942	Human LIPE gene po
c 173	14.6	1.5	15	1	ABK95979	Human LIPE gene po
174	14.6	1.5	15	1	ABK95940	Human LIPE gene po
c 175	14.6	1.5	15	1	ABK95973	Human LIPE gene po
176	14.6	1.5	15	1	ABK95944	Human LIPE gene po
177	14.4	1.5	16	1	ABL42981	Human chromosome 1
178	14.4	1.5	16	1	ABL44647	Human chromosome 1
c 179	14.4	1.5	17	1	AAH95977	Human Chk1 ribozym
c 180	14.4	1.5	17	1	AAH95352	Human Chk1 ribozym
c 181	14.4	1.5	17	1	AAH95217	Human Chk1 ribozym
182	14.4	1.5	17	1	ABK03125	Human CD20 Inozyme
183	14.4	1.5	17	1	ABN07602	Human GDMLP-1 17-m
184	14.4	1.5	17	1	ABN07599	Human GDMLP-1 17-m
c 185	14.4	1.5	17	1	ABN07714	Human GDMLP-1 17-m
c 186	14.4	1.5	17	1	ABN07713	Human GDMLP-1 17-m
c 187	14.4	1.5	17	1	ABV91100	Human POSHL1 scann
c 188	14.4	1.5	17	1	ABV91104	Human POSHL1 scann
189	14.4	1.5	17	1	ACC64755	Murine oligonucleo
c 190	14.4	1.5	17	1	ADB39860	Tumour suppression
c 191	14.4	1.5	17	1	ADB45011	Tumour suppression
192	14.4	1.5	17	1	ACC52389	Human tumour suppr
c 193	14.4	1.5	17	1	ACN70803	Human GDMLP-1 prob
c 194	14.4	1.5	17	1	ACN70804	Human GDMLP-1 prob
195	14.4	1.5	17	1	ACN70692	Human GDMLP-1 prob
196	14.4	1.5	17	1	ACN70689	Human GDMLP-1 prob
197	14.4	1.5	18	1	ADH28096	Human chromosome 1
198	14.4	1.5	19	1	AAA83522	cdk8 ribozyme bind
199	14.4	1.5	19	1	AAH58684	Cell-cycle depende
c 200	14.4	1.5	19	1	ADN34615	siNA upper strand
201	14.4	1.5	19	1	ADN34873	siNA lower strand
202	14.4	1.5	19	1	ADQ61607	Anti-RBBP2 siRNA r
203	14.4	1.5	20	1	AAQ91018	Primer binding to
c 204	14.4	1.5	20	1	AAX96757	PCR primer used to
c 205	14.4	1.5	20	1	AAD01299	M13 reverse primer
c 206	14.4	1.5	20	1	AAF23198	Oligonucleotide fo
c 207	14.4	1.5	20	1	AAF82542	Human PIK-related
c 208	14.4	1.5	20	1	ABK68858	Ehrlichia canis p2
c 209	14.4	1.5	20	1	ABT12957	Mycobacterium tube
210	14.4	1.5	20	1	AAL61452	Human ATF3 antisen
c 211	14.4	1.5	20	1	AAD49360	Mouse phospholipid
212	14.4	1.5	20	1	ADC36197	Weed controller me
213	14.4	1.5	20	1	ADG86932	Mouse PPAR antisen
c 214	14.4	1.5	20	1	ADH48268	Human GRK6 DNA, an
215	14.4	1.5	20	1	ADH48322	Human GRK6 DNA tar
216	14.4	1.5	20	1	ADI26626	Rat PIM1 antisense
217	14.4	1.5	20	1	ADJ32481	Human hypothetical
218	14.4	1.5	20	1	ADJ32489	Human hypothetical
219	14.4	1.5	20	1	ADK97560	Primer of the inve
c 220	14.4	1.5	20	1	ADJ19206	Antisense 2-MOE ga
221	14.4	1.5	20	1	ADL34870	Antisense oligonuc
c 222	14.4	1.5	20	1	ADO54491	Farnesoid X recept
c 223	14.4	1.5	20	1	ADO54502	Farnesoid X recept
c 224	14.4	1.5	20	1	ADO54521	Farnesoid X recept
c 225	14.4	1.5	20	1	ADO54079	Farnesoid X recept
c 226	14.4	1.5	20	1	ADO54698	Farnesoid X recept
227	14.4	1.5	20	1	ADN30061	Human cytokine-ind
228	14.2	1.5	19	1	AAZ20890	Primer 2 for detec
229	14.2	1.5	19	1	AAZ70164	Human biallelic ma
230	14.2	1.5	19	1	ABL88897	HIV-1 related bind
231	14.2	1.5	19	1	ADG35438	HIV siNA oligonucl
c 232	14.2	1.5	19	1	ADG36176	HIV siNA oligonucl
233	14.2	1.5	19	1	ADH16553	Human BACE siNA lo
c 234	14.2	1.5	19	1	ADH16228	Human BACE transcr
c 235	14.2	1.5	19	1	ADQ61805	Anti-PPARA siRNA r
236	14.2	1.5	19	1	ADQ31093	Cyp1A1 mRNA detect
c 237	14.2	1.5	20	1	AAQ33001	Probe for Chlamydi
238	14.2	1.5	20	1	AAQ75134	E.carotovora nucle
239	14.2	1.5	20	1	AAQ75225	Amino labelled oli
240	14.2	1.5	20	1	AAT48180	Primer CRYR, for i
c 241	14.2	1.5	20	1	AAX61144	Human chromosome a
242	14.2	1.5	20	1	AAZ05528	PCR primer used to
c 243	14.2	1.5	20	1	AAZ02129	PCR primer used to
244	14.2	1.5	20	1	AAZ03678	PCR primer used to
245	14.2	1.5	20	1	AAZ33908	Human PRO300 PCR f
c 246	14.2	1.5	20	1	AAX93212	PCR primer used to
c 247	14.2	1.5	20	1	AAX95409	PCR primer used to
248	14.2	1.5	20	1	AAX95679	PCR primer used to
c 249	14.2	1.5	20	1	AAX93272	PCR primer used to
c 250	14.2	1.5	20	1	AAX80212	Human CSF-1 antise
251	14.2	1.5	20	1	AAZ93692	Primer for amplify
252	14.2	1.5	20	1	AAA40712	Hamster DHFR gene

c 253	14.2	1.5	20	1	AAZ43821	Human fetal brain
254	14.2	1.5	20	1	AAZ29101	Forward primer new
255	14.2	1.5	20	1	AAA88539	Human GFR-alpha-3
256	14.2	1.5	20	1	AAC78613	Human PRO300 forwa
257	14.2	1.5	20	1	AAA77618	Human PRO538 PCR p
c 258	14.2	1.5	20	1	AAA49210	Human tumour necro
259	14.2	1.5	20	1	AAA54098	Primer for amplify
260	14.2	1.5	20	1	AAC58151	Human PRO538 and P
261	14.2	1.5	20	1	AAF87024	Sequencing primer
262	14.2	1.5	20	1	AAF30531	PPAR-alpha gene ex
263	14.2	1.5	20	1	AAH20646	Human telomeric re
c 264	14.2	1.5	20	1	AAH80522	Oligonucleotide hy
c 265	14.2	1.5	20	1	AAH80523	Oligonucleotide hy
c 266	14.2	1.5	20	1	ABA82191	Zmax1 gene region
c 267	14.2	1.5	20	1	AAD36541	Human Her-1 antise
c 268	14.2	1.5	20	1	ABL52377	Mouse FLIP-c chime
c 269	14.2	1.5	20	1	AAD38112	Human BCAS1 antise
c 270	14.2	1.5	20	1	AAL49434	Cell adhesion mole
c 271	14.2	1.5	20	1	AAL49432	Cell adhesion mole
c 272	14.2	1.5	20	1	ABQ81631	PGHS-2 sense prime
c 273	14.2	1.5	20	1	ABQ81627	PGHS-1 sense prime
c 274	14.2	1.5	20	1	ABL45275	Human chromosome 1
275	14.2	1.5	20	1	ABK43387	Siglec-BMS, PCR pr
276	14.2	1.5	20	1	ABI93019	Capture oligonucle
277	14.2	1.5	20	1	ACA63476	Novel human secret
c 278	14.2	1.5	20	1	ABT34154	Human short hetero
279	14.2	1.5	20	1	ACA71640	Human PRO polypept
280	14.2	1.5	20	1	ABX92280	Human PRO DNA PCR
281	14.2	1.5	20	1	ACA66021	Human secreted/tra
282	14.2	1.5	20	1	ABT15981	HIV variant detect
283	14.2	1.5	20	1	ADA24560	Secreted and trans
284	14.2	1.5	20	1	ACD29622	Novel human secret
285	14.2	1.5	20	1	ADA12221	Human secreted/tra
286	14.2	1.5	20	1	ACD29037	Novel human secret
287	14.2	1.5	20	1	ADB65822	Clone specific PCR
288	14.2	1.5	20	1	ADB73527	Human PRO DNA PCR
289	14.2	1.5	20	1	ADB76243	Human PRO DNA PCR
290	14.2	1.5	20	1	ADC43669	Human PRO 300 PCR
291	14.2	1.5	20	1	ADC61429	Human PRO 300 PCR
292	14.2	1.5	20	1	ADC63393	Human PRO 300 PCR
293	14.2	1.5	20	1	ADC66493	Human PRO 300 PCR
294	14.2	1.5	20	1	ADC68617	Human PRO 300 PCR
295	14.2	1.5	20	1	ADC62677	Human PRO 300 PCR
296	14.2	1.5	20	1	ADC67742	Human PRO 300 PCR
297	14.2	1.5	20	1	ADC41062	Human PRO 300 PCR
298	14.2	1.5	20	1	ADC67117	Human PRO 300 PCR
299	14.2	1.5	20	1	ADC62053	Human PRO 300 PCR
300	14.2	1.5	20	1	ADC41686	Human PRO 300 PCR
301	14.2	1.5	20	1	ADE49055	Human PRO 300 PCR
c 302	14.2	1.5	20	1	ADD81414	HIV PRT antisense
c 303	14.2	1.5	20	1	ADD81413	HIV PRT antisense
304	14.2	1.5	20	1	ADE35109	Human PRO 300 PCR
305	14.2	1.5	20	1	ADE16223	Human PRO 300 PCR
306	14.2	1.5	20	1	ADD72838	Human PRO 300 PCR
307	14.2	1.5	20	1	ADD72196	Human PRO 300 PCR
c 308	14.2	1.5	20	1	ADE39914	PCR primer (SEQ ID
c 309	14.2	1.5	20	1	ADE39918	PCR primer (SEQ ID
310	14.2	1.5	20	1	ADE16847	Human PRO 300 PCR
311	14.2	1.5	20	1	ADF46861	Human PRO 300 PCR
312	14.2	1.5	20	1	ADG52618	Human PRO 300 PCR
313	14.2	1.5	20	1	ADG59938	Human PRO 300 PCR
314	14.2	1.5	20	1	ADI60698	Human PRO 300 PCR
c 315	14.2	1.5	20	1	ABZ91282	Human oligonucleot
316	14.2	1.5	20	1	ABZ93292	Human oligonucleot
c 317	14.2	1.5	20	1	ABZ93501	Human oligonucleot
318	14.2	1.5	20	1	ACD42441	Novel human secret
319	14.2	1.5	20	1	ADL24968	Intestinal epithel
320	14.2	1.5	20	1	ADL24868	Intestinal epithel
c 321	14.2	1.5	20	1	ABD29731	AA626698-derived o
c 322	14.2	1.5	20	1	ABD27512	AA486238-derived o
323	14.2	1.5	20	1	ABD29522	AA664176-derived o
324	14.2	1.5	20	1	ADE48355	Human PRO 300 PCR
325	14.2	1.5	20	1	ADE89456	Human PRO 300 PCR
326	14.2	1.5	20	1	ADF61096	Human PRO 300 PCR
327	14.2	1.5	20	1	ADF39788	Human PRO 300 PCR
328	14.2	1.5	20	1	ADF45584	Human PRO 300 PCR
329	14.2	1.5	20	1	ADF23980	Human PRO 300 PCR
330	14.2	1.5	20	1	ADF40412	Human PRO 300 PCR
331	14.2	1.5	20	1	ADF23356	Human PRO 300 PCR
332	14.2	1.5	20	1	ADF33339	Human PRO 300 PCR
333	14.2	1.5	20	1	ADF26806	Human PRO 300 PCR
334	14.2	1.5	20	1	ADF27442	Human PRO 300 PCR
335	14.2	1.5	20	1	ADF41036	Human PRO 300 PCR
336	14.2	1.5	20	1	ADF32715	Human PRO 300 PCR
337	14.2	1.5	20	1	ADF25081	Human PRO 300 PCR
338	14.2	1.5	20	1	ADF26182	Human PRO 300 PCR
339	14.2	1.5	20	1	ADF33971	Human PRO 300 PCR
340	14.2	1.5	20	1	ADF46208	Human PRO 300 PCR
341	14.2	1.5	20	1	ADG50194	Human PRO 300 PCR
342	14.2	1.5	20	1	ADG49570	Human PRO 300 PCR
343	14.2	1.5	20	1	ADG51442	Human PRO 300 PCR
344	14.2	1.5	20	1	ADG48946	Human PRO 300 PCR
345	14.2	1.5	20	1	ADG48322	Human PRO 300 PCR
346	14.2	1.5	20	1	ADG84982	MSH6 gene-specific
347	14.2	1.5	20	1	ADG50818	Human PRO 300 PCR
348	14.2	1.5	20	1	ADG58762	Human PRO 300 PCR
349	14.2	1.5	20	1	ADG62218	Human PRO 300 PCR
350	14.2	1.5	20	1	ADH63981	Human glucocortico
c 351	14.2	1.5	20	1	ADH65573	Human glucocortico
352	14.2	1.5	20	1	ADH63740	Human glucocortico
c 353	14.2	1.5	20	1	ADH66186	Human glucocortico
354	14.2	1.5	20	1	ADI80213	Human transforming
c 355	14.2	1.5	20	1	ADI80073	Human transforming
356	14.2	1.5	20	1	ADH89600	Human Livin antise
357	14.2	1.5	20	1	ADH25243	Human neurotrimin
c 358	14.2	1.5	20	1	ADJ78447	Human perilipin ta
359	14.2	1.5	20	1	ADJ78377	Human perilipin ch
c 360	14.2	1.5	20	1	ADJ18101	Antisense DNA olig
c 361	14.2	1.5	20	1	ADJ18234	Antisense DNA olig
c 362	14.2	1.5	20	1	ADJ18569	Antisense DNA olig
c 363	14.2	1.5	20	1	ADJ18514	Antisense DNA olig
c 364	14.2	1.5	20	1	ADK76897	Chimeric phosphoro
c 365	14.2	1.5	20	1	ADK75814	Chimeric phosphoro
c 366	14.2	1.5	20	1	ADK76483	Chimeric phosphoro
c 367	14.2	1.5	20	1	ADK75654	Chimeric phosphoro
368	14.2	1.5	20	1	ADM17020	Human PRO 300 PCR
369	14.2	1.5	20	1	ADL06854	Human PRO 300 PCR
370	14.2	1.5	20	1	ADM14424	Human mPGES-1 chim
371	14.2	1.5	20	1	ADM14626	Human mPGES-1 chim
372	14.2	1.5	20	1	ADO54308	Farnesoid X recept
373	14.2	1.5	20	1	ADO54014	Farnesoid X recept
c 374	14.2	1.5	20	1	ADN03090	Human PIM-1 DNA an
c 375	14.2	1.5	20	1	ADN03079	Human PIM-1 DNA an
376	14.2	1.5	20	1	ADN03148	Human PIM-1 DNA an
377	14.2	1.5	20	1	ADO16801	4 synthesis-period
c 378	14.2	1.5	20	1	ADP78345	Chimeric phosphoro
c 379	14.2	1.5	20	1	ADP78490	Chimeric phosphoro
380	14.2	1.5	20	1	ADN30196	Hepatocyte growth
c 381	14.2	1.5	20	1	ADN30267	Hepatocyte growth
382	14.2	1.5	20	1	ADP27889	PCR primer to ampl
383	14.2	1.5	20	1	ADP74452	Human NRF antisens
c 384	14.2	1.5	20	1	ADP74522	Human NRF antisens
385	14.2	1.5	20	1	ADR00341	RIZ1 PCR reverse p
c 386	14.2	1.5	20	1	ADK20894	Acyl-coenzyme A sy
c 387	14.2	1.5	20	1	ADK22640	Acyl-coenzyme A sy
c 388	14.2	1.5	20	1	ADK23097	Acyl-coenzyme A sy
c 389	14.2	1.5	20	1	ADK21310	Acyl-coenzyme A sy
c 390	14.2	1.5	20	1	ADR86633	Human HCN4 gene ex
391	14.2	1.5	20	1	ADT00460	Novel mutant prote
392	14.2	1.5	20	1	ADT00459	Novel mutant prote
393	14.2	1.5	20	1	ADT94303	Human PRO538 cDNA
394	14	1.4	14	1	ADR44875	G3PDH gene PCR pri
395	14	1.4	15	1	AAV18733	Primer for HRSV gl
396	14	1.4	17	1	ABN07597	Human GDMLP-1 17-m
397	14	1.4	17	1	ABN07598	Human GDMLP-1 17-m
c 398	14	1.4	17	1	ABN07711	Human GDMLP-1 17-m

c 399	14	1.4	17	1	ABN07712	Human GDMLP-1 17-m
400	14	1.4	17	1	ACC66338	Murine oligonucleo
c 401	14	1.4	17	1	ACN70802	Human GDMLP-1 prob
c 402	14	1.4	17	1	ACN70801	Human GDMLP-1 prob
403	14	1.4	17	1	ACN70688	Human GDMLP-1 prob
404	14	1.4	17	1	ACN70687	Human GDMLP-1 prob
405	14	1.4	18	1	AAT50908	Probe SH-10 for HS
406	14	1.4	18	1	AAT70004	Probe SH-10 for HS
c 407	14	1.4	18	1	AAX54836	C/EBP-beta antisen
c 408	14	1.4	18	1	AAA34283	Human adenosine re
c 409	14	1.4	18	1	AAF20405	Human C/EBP polynu
c 410	14	1.4	18	1	ABZ96099	Human C/EBP antise
c 411	14	1.4	19	1	AAX54835	C/EBP-beta antisen
c 412	14	1.4	19	1	AAA34282	Human adenosine re
c 413	14	1.4	19	1	AAF20404	Human C/EBP polynu
c 414	14	1.4	19	1	ABZ96098	Human C/EBP antise
c 415	14	1.4	19	1	ADR75648	Human apolipoprote
c 416	14	1.4	19	1	ADR75888	Human apolipoprote
c 417	14	1.4	19	1	ADR78266	Human apolipoprote
c 418	14	1.4	19	1	ADR78506	Human apolipoprote
c 419	14	1.4	20	1	AAX54834	C/EBP-beta antisen
c 420	14	1.4	20	1	AAX92068	PCR primer used to
c 421	14	1.4	20	1	AAA34281	Human adenosine re
c 422	14	1.4	20	1	AAA40869	Murine TNFalpha an
c 423	14	1.4	20	1	AAF20403	Human C/EBP polynu
c 424	14	1.4	20	1	ACD05097	Tumour necrosis fa
c 425	14	1.4	20	1	ADF42478	Primer for amplify
c 426	14	1.4	20	1	ABZ85209	Human oligonucleot
c 427	14	1.4	20	1	ABZ96097	Human C/EBP antise
c 428	14	1.4	20	1	ABD21439	Human transglutami
429	14	1.4	20	1	ADP27278	Human MMP11 DNA an
c 430	14	1.4	20	1	ADP27133	Human matrix metal
c 431	14	1.4	20	1	ADQ29179	Mouse TNF alpha an
c 432	14	1.4	20	1	ADR02695	Antisense oligonuc
c 433	13.8	1.4	17	1	AAX62853	Delta-9 desaturase
434	13.8	1.4	17	1	AAA36167	Human genomic SNP
435	13.8	1.4	17	1	ABK03691	Human CD20 Amberzy
436	13.8	1.4	17	1	ABK03692	Human CD20 Amberzy
437	13.8	1.4	17	1	ABL46609	Human GRID NCH rib
438	13.8	1.4	17	1	ABL47134	Human GRID Amberzy
439	13.8	1.4	17	1	ABN07596	Human GDMLP-1 17-m
440	13.8	1.4	17	1	ABN00495	Human GDMLP-1 17-m
441	13.8	1.4	17	1	ABN07595	Human GDMLP-1 17-m
c 442	13.8	1.4	17	1	ABN07715	Human GDMLP-1 17-m
c 443	13.8	1.4	17	1	ABN07716	Human GDMLP-1 17-m
444	13.8	1.4	17	1	ABQ63739	Human KTOM1a porti
445	13.8	1.4	17	1	ABT36354	Tumour suppression
c 446	13.8	1.4	17	1	ACA09002	NFKB sub-unit modu
c 447	13.8	1.4	17	1	ACA09005	NFKB sub-unit modu
c 448	13.8	1.4	17	1	ACA06538	NFKB sub-unit modu
449	13.8	1.4	17	1	ADB00052	Human MDZ3 scannin
450	13.8	1.4	17	1	ADB00053	Human MDZ3 scannin
451	13.8	1.4	17	1	ADB00054	Human MDZ3 scannin
452	13.8	1.4	17	1	ACC65263	Murine oligonucleo
c 453	13.8	1.4	17	1	ACC64648	Murine oligonucleo
454	13.8	1.4	17	1	ACC63630	Murine oligonucleo
455	13.8	1.4	17	1	ACC63843	Murine oligonucleo
c 456	13.8	1.4	17	1	ACC63438	Murine oligonucleo
457	13.8	1.4	17	1	ADB40040	Tumour suppression
458	13.8	1.4	17	1	ADB41320	Tumour suppression
459	13.8	1.4	17	1	ADI50598	Human tumour suppr
460	13.8	1.4	17	1	ADI49425	Human tumour suppr
c 461	13.8	1.4	17	1	ADI49372	Human tumour suppr
c 462	13.8	1.4	17	1	ABX13141	Rat p11 mutagenic
463	13.8	1.4	17	1	ADM53967	Human GRID mRNA su
464	13.8	1.4	17	1	ACN63585	Human GDMLP-1 prob
c 465	13.8	1.4	17	1	ACN70806	Human GDMLP-1 prob
466	13.8	1.4	17	1	ACN70685	Human GDMLP-1 prob
467	13.8	1.4	17	1	ACN70686	Human GDMLP-1 prob
c 468	13.8	1.4	17	1	ACN70805	Human GDMLP-1 prob
469	13.8	1.4	17	1	ADR74696	Common primer for
c 470	13.8	1.4	18	1	AAT39740	rev-AS (2328) anti
c 471	13.8	1.4	18	1	AAT43031	Juvenile glaucoma
c 472	13.8	1.4	18	1	AAT51719	Oligonucleotide 26
473	13.8	1.4	18	1	AAH47533	Human Her-3 mRNA i
474	13.8	1.4	18	1	ACF62765	Colon cancer analy
c 475	13.8	1.4	18	1	ACF62766	Colon cancer analy
c 476	13.8	1.4	18	1	ADM06739	Human PCR primer S
c 477	13.8	1.4	18	1	ABD20008	Human C/EBPN DNA f
478	13.8	1.4	18	1	ADH36252	Human purinergic r
c 479	13.8	1.4	19	1	AAT76395	Human tumour necro
480	13.8	1.4	19	1	AAV08200	PCR primer ABCR.EX
481	13.8	1.4	19	1	AAV08220	PCR primer ABCR.EX
c 482	13.8	1.4	19	1	AAV72612	Glucose-6-phosphat
c 483	13.8	1.4	19	1	AAX56380	DNA-dependent ATPa
c 484	13.8	1.4	19	1	AAX54544	Human adenosine A2
c 485	13.8	1.4	19	1	AAA33988	Low adenosine anti
486	13.8	1.4	19	1	AAA83068	cdk6 ribozyme bind
c 487	13.8	1.4	19	1	AAA83572	cdk-we-hu ribozyme
488	13.8	1.4	19	1	AAA86016	Cdc 25 hs ribozyme
489	13.8	1.4	19	1	AAA84481	Cyclin E ribozyme
c 490	13.8	1.4	19	1	AAF20110	Human tumour necro
491	13.8	1.4	19	1	AAH58230	Cell-cycle depende
c 492	13.8	1.4	19	1	AAH58734	Cdk-we-hu ribozyme
493	13.8	1.4	19	1	AAH61178	Cdc25 hs ribozyme
494	13.8	1.4	19	1	AAH59643	Cyclin E ribozyme
c 495	13.8	1.4	19	1	ADA25500	Human PKC-alpha sh
496	13.8	1.4	19	1	ADA25375	Human PKC-alpha sh
c 497	13.8	1.4	19	1	ADE29876	Mitogen activated
498	13.8	1.4	19	1	ADE29771	Mitogen activated
499	13.8	1.4	19	1	ADE30306	Mitogen activated
c 500	13.8	1.4	19	1	ADE30097	Mitogen activated
c 501	13.8	1.4	19	1	ADF39624	C8ORF4 gene antise
c 502	13.8	1.4	19	1	ADF75719	Antisense siNA tha
503	13.8	1.4	19	1	ADF75534	Sense siNA that do
504	13.8	1.4	19	1	ADG35531	HIV siNA oligonucl
505	13.8	1.4	19	1	ADG35292	HIV siNA oligonucl
c 506	13.8	1.4	19	1	ADG36269	HIV siNA oligonucl
c 507	13.8	1.4	19	1	ADG36030	HIV siNA oligonucl
c 508	13.8	1.4	19	1	ABZ95804	Human tumour necro
c 509	13.8	1.4	19	1	ABD20007	Human C/EBPN DNA f
c 510	13.8	1.4	19	1	ABD19544	Human tumour necro
511	13.8	1.4	19	1	ADO22943	Human sequence con
512	13.8	1.4	19	1	ADQ62407	Anti-GTSE1 siRNA S
c 513	13.6	1.4	15	1	ABK95977	Human LIPE gene po
c 514	13.6	1.4	16	1	AAX54838	C/EBP-beta antisen
c 515	13.6	1.4	16	1	AAA34285	Human adenosine re
c 516	13.6	1.4	16	1	AAF20407	Human C/EBP polynu
c 517	13.6	1.4	16	1	ABZ96101	Human C/EBP antise
c 518	13.6	1.4	17	1	AAX54837	C/EBP-beta antisen
c 519	13.6	1.4	17	1	AAA34284	Human adenosine re
c 520	13.6	1.4	17	1	AAF20406	Human C/EBP polynu
c 521	13.6	1.4	17	1	ABZ96100	Human C/EBP antise
522	13.6	1.4	20	1	ABZ99357	Human PDE4C oligon
523	13.6	1.4	20	1	ABD32388	Human PDE4C-derive
524	13.6	1.4	20	1	ADJ61242	Oligonucleotide as
525	13.6	1.4	20	1	ADO46632	Human oligonucleot
c 526	13.4	1.4	15	1	AAC73366	Reverse primer #74
c 527	13.4	1.4	15	1	AAF46427	IGFBP2 oligonucleo
528	13.4	1.4	16	1	AAA97434	Gluconobacter oxyd
c 529	13.4	1.4	16	1	ABD20010	Human C/EBPN DNA f
c 530	13.4	1.4	17	1	AAT81209	Human c-myb hammer
531	13.4	1.4	17	1	AAX74793	Mouse flt-1 VEGF r
532	13.4	1.4	17	1	AAX74957	Mouse flt-1 VEGF r
c 533	13.4	1.4	17	1	AAX75320	Mouse flt-1 VEGF r
534	13.4	1.4	17	1	AAX74956	Mouse flt-1 VEGF r
535	13.4	1.4	17	1	AAV97492	Human EGF-R target
536	13.4	1.4	17	1	AAX57838	PCR primer for G.
c 537	13.4	1.4	17	1	AAH95216	Human Chk1 ribozym
538	13.4	1.4	17	1	ABK03469	Human CD20 Zinzyme
c 539	13.4	1.4	17	1	AAH91135	Human inflammatory
540	13.4	1.4	17	1	ABN07603	Human GDMLP-1 17-m
541	13.4	1.4	17	1	ABN00494	Human GDMLP-1 17-m
542	13.4	1.4	17	1	ABN00493	Human GDMLP-1 17-m
543	13.4	1.4	17	1	ABQ63741	Human KTOM1a porti
544	13.4	1.4	17	1	ABQ63740	Human KTOM1a porti

c	545	13.4	1.4	17	1	ABV91099	Human POSHL1 scann
c	546	13.4	1.4	17	1	ABV91105	Human POSHL1 scann
	547	13.4	1.4	17	1	ABT37970	Tumour suppression
c	548	13.4	1.4	17	1	ABT38045	Tumour suppression
	549	13.4	1.4	17	1	ABT39267	Tumour suppression
c	550	13.4	1.4	17	1	ABZ61864	Human H-Ras DNAzym
c	551	13.4	1.4	17	1	ABZ61330	Human H-Ras DNAzym
c	552	13.4	1.4	17	1	ACC66009	Murine oligonucleo
c	553	13.4	1.4	17	1	ACC64573	Murine oligonucleo
c	554	13.4	1.4	17	1	ACC64668	Murine oligonucleo
c	555	13.4	1.4	17	1	ADB98975	LRP5 mutagenic PCR
c	556	13.4	1.4	17	1	ADB41073	Tumour suppression
	557	13.4	1.4	17	1	ADB43229	Tumour suppression
	558	13.4	1.4	17	1	ADB40679	Tumour suppression
c	559	13.4	1.4	17	1	ADB44571	Tumour suppression
	560	13.4	1.4	17	1	ADI51271	Human tumour suppr
	561	13.4	1.4	17	1	ACC52645	Human tumour suppr
c	562	13.4	1.4	17	1	ABD20009	Human C/EBPN DNA f
	563	13.4	1.4	17	1	ACN70693	Human GDMLP-1 prob
	564	13.4	1.4	17	1	ACN63584	Human GDMLP-1 prob
	565	13.4	1.4	17	1	ACN63583	Human GDMLP-1 prob
	566	13.4	1.4	18	1	AAT50609	Human CETP hairpin
	567	13.4	1.4	18	1	AAT50708	Rabbit CETP hairpi
	568	13.4	1.4	18	1	AAZ73000	Human biallelic ma
c	569	13.4	1.4	18	1	AAZ75130	Human biallelic ma
	570	13.4	1.4	18	1	AAA52046	Antisense oligonuc
	571	13.4	1.4	18	1	AAD41001	Human PI3K p85 ant
c	572	13.4	1.4	18	1	ABT12998	Human cytochrome C
	573	13.4	1.4	18	1	AAL55147	PGC-1 mutational a
	574	13.4	1.4	18	1	ADM06576	Human PCR primer S
	575	13.4	1.4	18	1	ADM06437	Human PCR primer S
c	576	13.4	1.4	18	1	ADJ38158	Plastid division-r
c	577	13.4	1.4	19	1	AAA82434	cdk1 ribozyme bind
	578	13.4	1.4	19	1	AAF87029	Sequencing primer
c	579	13.4	1.4	19	1	AAH37681	SNP specific upper
c	580	13.4	1.4	19	1	AAH57596	Cell-cycle depende
c	581	13.4	1.4	19	1	ABZ76184	A. thaliana metall
	582	13.4	1.4	19	1	ACH66601	Sense PCR primer u
	583	13.4	1.4	19	1	ADF37451	Human VEGFR3 short
c	584	13.4	1.4	19	1	ADF37698	Human VEGFR3 short
	585	13.4	1.4	19	1	ADH16597	Human BACE siNA lo
c	586	13.4	1.4	19	1	ADH16272	Human BACE transcr
	587	13.4	1.4	19	1	ABV75390	TGFB1 promoter T(-
	588	13.4	1.4	19	1	ADO14856	Human PDGFr-target
c	589	13.4	1.4	19	1	ADO15167	Human PDGFr-target
c	590	13.4	1.4	19	1	ADH01971	Protein tyrosine p
	591	13.4	1.4	19	1	ADQ27669	RNA interference t
	592	13.2	1.4	18	1	AAQ41367	Monomer DRB1002 fo
	593	13.2	1.4	18	1	AAQ55068	Sequence of fragme
c	594	13.2	1.4	18	1	AAT56750	Mouse TNF-alpha ha
c	595	13.2	1.4	18	1	AAV02860	Human HMGI-C gene
c	596	13.2	1.4	18	1	AAV14198	Probe HBPr93 for g
	597	13.2	1.4	18	1	AAX03785	Human C5 antisense
	598	13.2	1.4	18	1	AAZ40992	Human RhoC phospho
c	599	13.2	1.4	18	1	AAZ44132	Human EGR-1 DNA an
c	600	13.2	1.4	18	1	AAZ72009	Human biallelic ma
	601	13.2	1.4	18	1	AAA52269	Human C5 antisense
	602	13.2	1.4	18	1	AAA99734	Human C5 gene anti
	603	13.2	1.4	18	1	AAZ93479	TRADD antisense ol
	604	13.2	1.4	18	1	AAF79609	Human Akt-3 antise
	605	13.2	1.4	18	1	AAF94713	Rho C antisense ph
c	606	13.2	1.4	18	1	AAD09729	ZC26415 PCR primer
	607	13.2	1.4	18	1	ABA82519	Zmax1 gene region
	608	13.2	1.4	18	1	ABK23316	Human Zmax1 cDNA r
	609	13.2	1.4	18	1	ABT06049	Human IgM heavy ch
	610	13.2	1.4	18	1	ABT06048	Human IgM heavy ch
	611	13.2	1.4	18	1	ABL30592	Human HLA genotypi
	612	13.2	1.4	18	1	AAD41287	Human C6ST gene am
c	613	13.2	1.4	18	1	ABZ74876	Human carnitine tr
	614	13.2	1.4	18	1	ACC45899	Human HBM STS mark
	615	13.2	1.4	18	1	ACD19636	Human obesity rela
	616	13.2	1.4	18	1	ADB98597	Sequence tagged si
c	617	13.2	1.4	18	1	ADC02807	Ex vivo stem-cell
	618	13.2	1.4	18	1	ADD26423	Human BCR intron 1
c	619	13.2	1.4	18	1	ACF58297	Human IL-TIF cDNA
c	620	13.2	1.4	18	1	ADH69529	PCR primer ZC26415
c	621	13.2	1.4	18	1	ABT23665	Stabilising reagen
	622	13.2	1.4	18	1	ABT23656	Stabilising reagen
c	623	13.2	1.4	18	1	ADI58482	Human interleukin
c	624	13.2	1.4	18	1	ADM69761	Plant gene polymor
	625	13.2	1.4	18	1	ADR17462	Human chromosome 1
	626	13.2	1.4	18	1	ADR48113	Human chromosome 1
c	627	13	1.3	13	1	AAA26826	Trichosporon sp po
	628	13	1.3	13	1	ABF28359	Oligonucleotide SE
c	629	13	1.3	13	1	ABF28358	Oligonucleotide SE
c	630	13	1.3	15	1	ABK95764	Solute Carrier Fam
	631	13	1.3	15	1	ABK95976	Human LIPE gene po
	632	13	1.3	15	1	ABK95943	Human LIPE gene po
c	633	13	1.3	16	1	ADS91058	Oligonucleotide of
c	634	13	1.3	17	1	AAT81210	Human c-myb hammer
c	635	13	1.3	17	1	AAT60343	Forward primer for
c	636	13	1.3	17	1	AAA36322	Human genomic SNP
c	637	13	1.3	17	1	AAH94857	Human Chk1 ribozym
c	638	13	1.3	17	1	AAH94858	Human Chk1 ribozym
c	639	13	1.3	17	1	ABN07710	Human GDMLP-1 17-m
c	640	13	1.3	17	1	ACN07867	WNV minus strand H
c	641	13	1.3	17	1	ACN12552	WNV minus strand Z
c	642	13	1.3	17	1	ACN10138	WNV minus strand I
	643	13	1.3	17	1	ACN03003	WNV Inozyme substr
	644	13	1.3	17	1	ACN05307	WNV DNAzyme substr
	645	13	1.3	17	1	ACN03002	WNV Inozyme substr
c	646	13	1.3	17	1	ACN14428	WNV minus strand A
	647	13	1.3	17	1	ABT39774	Tumour suppression
c	648	13	1.3	17	1	ABT38307	Tumour suppression
c	649	13	1.3	17	1	ACA06536	NFKB sub-unit modu
c	650	13	1.3	17	1	ACA06537	NFKB sub-unit modu
c	651	13	1.3	17	1	ADB42638	Tumour suppression
	652	13	1.3	17	1	ADB45962	Tumour suppression
	653	13	1.3	17	1	ADE48000	Human NOVX reverse
c	654	13	1.3	17	1	ADI48149	Human tumour suppr
c	655	13	1.3	17	1	ABQ84437	DPP10 PCR primer #
	656	13	1.3	17	1	ADJ79270	Human NOVX protein
	657	13	1.3	17	1	ADK13409	Human glioma endot
	658	13	1.3	17	1	ADK13120	Human glioma endot
c	659	13	1.3	17	1	ADO42100	Short tandem repea
c	660	13	1.3	17	1	ACN70800	Human GDMLP-1 prob
	661	13	1.3	18	1	ABL31588	Human HLA genotypi
	662	13	1.3	18	1	ACC83808	Glyceraldehyde 3-p
c	663	13	1.3	18	1	ADP46379	Extend primer 8 us
c	664	12.8	1.3	16	1	AAQ95946	Primer B (Group 13
c	665	12.8	1.3	16	1	ADR43841	Human thioredoxin
	666	12.8	1.3	16	1	ADR70003	Human survivin gen
c	667	12.8	1.3	17	1	AAX75131	Mouse flt-1 VEGF r
c	668	12.8	1.3	17	1	AAX62852	Delta-9 desaturase
	669	12.8	1.3	17	1	AAV94636	Human IL-2 recepto
c	670	12.8	1.3	17	1	AAX33137	Beta-galactosidase
	671	12.8	1.3	17	1	AAA24932	Oestrogen receptor
	672	12.8	1.3	17	1	AAF02649	Hammerhead ribozym
c	673	12.8	1.3	17	1	AAF07119	Hammerhead ribozym
	674	12.8	1.3	17	1	AAF01952	Hammerhead ribozym
c	675	12.8	1.3	17	1	AAF03081	Hammerhead ribozym
	676	12.8	1.3	17	1	AAF07020	Hammerhead ribozym
c	677	12.8	1.3	17	1	AAF03080	Hammerhead ribozym
	678	12.8	1.3	17	1	ABK03693	Human CD20 Amberzy
c	679	12.8	1.3	17	1	ABA78473	CFTR mutation corr
	680	12.8	1.3	17	1	ABA78474	CFTR mutation corr
	681	12.8	1.3	17	1	ABL46608	Human GRID NCH rib
c	682	12.8	1.3	17	1	ABL47070	Human GRID DNAzyme
	683	12.8	1.3	17	1	ABL47135	Human GRID Amberzy
c	684	12.8	1.3	17	1	ABL47200	Human GRID Amberzy
	685	12.8	1.3	17	1	ABL46823	Human GRID NCH rib
	686	12.8	1.3	17	1	ABL47093	Human GRID DNAzyme
c	687	12.8	1.3	17	1	AAF79904	Primer used to amp
	688	12.8	1.3	17	1	ABL92158	Long human Tumour
	689	12.8	1.3	17	1	ABL92157	Long human Tumour
c	690	12.8	1.3	17	1	ABN07717	Human GDMLP-1 17-m

	691	12.8	1.3	17	1	ABN07594	Human GDMLP-1 17-m
	692	12.8	1.3	17	1	ABN00496	Human GDMLP-1 17-m
	693	12.8	1.3	17	1	ABQ63738	Human KTOM1a porti
c	694	12.8	1.3	17	1	AAD24250	Mutagenic PCR prim
c	695	12.8	1.3	17	1	ABK19447	Human ERG Amberzym
c	696	12.8	1.3	17	1	ABK18886	Human ERG DNAzyme
c	697	12.8	1.3	17	1	ABK17494	Human ERG hammerhe
c	698	12.8	1.3	17	1	ABK17493	Human ERG hammerhe
c	699	12.8	1.3	17	1	ABL31707	Human HLA genotypi
c	700	12.8	1.3	17	1	ABK56151	Human CLCA1 gene e
	701	12.8	1.3	17	1	ABK56380	Human CLCA1 gene e
c	702	12.8	1.3	17	1	ABK56152	Human CLCA1 gene e
	703	12.8	1.3	17	1	ACN06328	WNV Amberzyme subs
c	704	12.8	1.3	17	1	ACN14786	WNV minus strand A
	705	12.8	1.3	17	1	ACN06329	WNV Amberzyme subs
c	706	12.8	1.3	17	1	ACN08557	WNV minus strand H
c	707	12.8	1.3	17	1	ACN12684	WNV minus strand Z
	708	12.8	1.3	17	1	ACN02796	WNV Inozyme substr
	709	12.8	1.3	17	1	ACN02364	WNV Inozyme substr
	710	12.8	1.3	17	1	ACN00700	WNV Hammerhead Rib
c	711	12.8	1.3	17	1	ACN10982	WNV minus strand I
	712	12.8	1.3	17	1	ABT36748	Tumour suppression
c	713	12.8	1.3	17	1	ABT35570	Tumour suppression
c	714	12.8	1.3	17	1	ACA07755	NFKB sub-unit modu
c	715	12.8	1.3	17	1	ACA06470	NFKB sub-unit modu
c	716	12.8	1.3	17	1	ACA06471	NFKB sub-unit modu
c	717	12.8	1.3	17	1	ACA06516	NFKB sub-unit modu
	718	12.8	1.3	17	1	ACA06464	NFKB sub-unit modu
c	719	12.8	1.3	17	1	ACA07747	NFKB sub-unit modu
	720	12.8	1.3	17	1	ADB05329	Human MDZ12 scanni
	721	12.8	1.3	17	1	ADB05330	Human MDZ12 scanni
	722	12.8	1.3	17	1	ADB00051	Human MDZ3 scannin
	723	12.8	1.3	17	1	ADB00055	Human MDZ3 scannin
	724	12.8	1.3	17	1	ADB02516	Human MDZ4 scannin
	725	12.8	1.3	17	1	ADB02515	Human MDZ4 scannin
c	726	12.8	1.3	17	1	ABZ61238	Human H-Ras DNAzym
c	727	12.8	1.3	17	1	ABZ59953	Human K-Ras DNAzym
c	728	12.8	1.3	17	1	ABZ59954	Human K-Ras DNAzym
c	729	12.8	1.3	17	1	ABZ65094	Human HER2 DNAzyme
c	730	12.8	1.3	17	1	ABZ65504	Human HER2 DNAzyme
	731	12.8	1.3	17	1	ABZ61654	Human H-Ras DNAzym
c	732	12.8	1.3	17	1	ABZ62204	Human H-Ras DNAzym
	733	12.8	1.3	17	1	ABZ64571	Human HER2 DNAzyme
c	734	12.8	1.3	17	1	ACD61605	HCV minus strand D
	735	12.8	1.3	17	1	ACD61063	HCV DNAzyme substr
	736	12.8	1.3	17	1	ACD61064	HCV DNAzyme substr
	737	12.8	1.3	17	1	ACD64618	HCV minus strand D
c	738	12.8	1.3	17	1	ACD61606	HCV minus strand D
	739	12.8	1.3	17	1	ACC66305	Murine oligonucleo
	740	12.8	1.3	17	1	ACC64234	Murine oligonucleo
c	741	12.8	1.3	17	1	ACC67719	Murine oligonucleo
c	742	12.8	1.3	17	1	ACC63436	Murine oligonucleo
c	743	12.8	1.3	17	1	ACC63442	Murine oligonucleo
	744	12.8	1.3	17	1	ACC63424	Murine oligonucleo
c	745	12.8	1.3	17	1	ACC64399	Murine oligonucleo
	746	12.8	1.3	17	1	ADB42193	Tumour suppression
	747	12.8	1.3	17	1	ADB42709	Tumour suppression
c	748	12.8	1.3	17	1	ADB41415	Tumour suppression
c	749	12.8	1.3	17	1	ADC03734	Human Na/H exchang
c	750	12.8	1.3	17	1	ADC03733	Human Na/H exchang
c	751	12.8	1.3	17	1	ADB45540	Tumour suppression
c	752	12.8	1.3	17	1	ADB44781	Tumour suppression
	753	12.8	1.3	17	1	ADB44421	Tumour suppression
	754	12.8	1.3	17	1	ADC98398	FST104 polymorphis
c	755	12.8	1.3	17	1	ADF64389	Human PCCP1 DNA fr
c	756	12.8	1.3	17	1	ADF64390	Human PCCP1 DNA fr
c	757	12.8	1.3	17	1	ADG70291	CLLD8 exon 12 and
	758	12.8	1.3	17	1	ADI52105	Human tumour suppr
	759	12.8	1.3	17	1	ADI50239	Human tumour suppr
	760	12.8	1.3	17	1	ADI49914	Human tumour suppr
	761	12.8	1.3	17	1	ACC52597	Human tumour suppr
	762	12.8	1.3	17	1	ACC53030	Human tumour suppr
	763	12.8	1.3	17	1	ACC52357	Human tumour suppr
	764	12.8	1.3	17	1	ABX72083	Human tumour endot
	765	12.8	1.3	17	1	ABX72082	Human tumour endot
	766	12.8	1.3	17	1	ADL47061	Human NOGO recepto
	767	12.8	1.3	17	1	ADL48439	Human IKK-gamma su
	768	12.8	1.3	17	1	ADL46632	Human NOGO recepto
c	769	12.8	1.3	17	1	ADL48316	Human IKK-gamma su
	770	12.8	1.3	17	1	ADL48867	Human IKK-gamma su
c	771	12.8	1.3	17	1	ADM54521	Human GRID mRNA su
	772	12.8	1.3	17	1	ADM53966	Human GRID mRNA su
	773	12.8	1.3	17	1	ADM54181	Human GRID mRNA su
	774	12.8	1.3	17	1	ADK13141	Human glioma endot
	775	12.8	1.3	17	1	ADI84891	HCV DNAzyme substr
c	776	12.8	1.3	17	1	ADI85172	HCV DNAzyme substr
c	777	12.8	1.3	17	1	ADI85171	HCV DNAzyme substr
	778	12.8	1.3	17	1	ADI86672	HCV DNAzyme substr
	779	12.8	1.3	17	1	ADL60409	Human organic anio
	780	12.8	1.3	17	1	ACN63586	Human GDMLP-1 prob
	781	12.8	1.3	17	1	ACN70684	Human GDMLP-1 prob
c	782	12.8	1.3	17	1	ACN70807	Human GDMLP-1 prob
	783	12.8	1.3	18	1	AAQ70337	Antisense oligonuc
c	784	12.8	1.3	18	1	AAQ82167	Chromosome 11 (loc
c	785	12.8	1.3	18	1	AAT28317	Multi-G oligonucle
	786	12.8	1.3	18	1	AAT28319	Multi-G oligonucle
	787	12.8	1.3	18	1	AAV08122	Primer Vbeta10 for
	788	12.8	1.3	18	1	AAV69398	H. contortus PGP-0
c	789	12.8	1.3	18	1	AAZ65577	Immunosuppressant
	790	12.8	1.3	18	1	AAA10573	Smad2 antisense ol
	791	12.8	1.3	18	1	AAZ69710	Human biallelic ma
c	792	12.8	1.3	18	1	AAA67055	Human leukocyte an
c	793	12.8	1.3	18	1	AAZ93477	TRADD antisense ol
c	794	12.8	1.3	18	1	AAF99483	Immunostimulatory
c	795	12.8	1.3	18	1	AAF99473	Immunostimulatory
	796	12.8	1.3	18	1	AAH47588	Human Her-3 mRNA i
c	797	12.8	1.3	18	1	AAF81096	Primer used to seq
	798	12.8	1.3	18	1	AAL49065	Drosophila ubx gen
	799	12.8	1.3	18	1	ABL53380	Insulin PCR primer
c	800	12.8	1.3	18	1	AAI70952	SPACERW oligonucle
c	801	12.8	1.3	18	1	AAI70968	Spacer used in CRC
c	802	12.8	1.3	18	1	ABS78144	Angiogenesis inhib
c	803	12.8	1.3	18	1	ABS78178	Angiogenesis inhib
c	804	12.8	1.3	18	1	ABL39063	Immunostimulatory
c	805	12.8	1.3	18	1	ABL39062	Immunostimulatory
	806	12.8	1.3	18	1	ABS60986	Human genotyping P
c	807	12.8	1.3	18	1	ABV72663	Human RISC forward
	808	12.8	1.3	18	1	ABS98043	Human multidrug re
c	809	12.8	1.3	18	1	ADG27380	Mouse Lpin2 gene 3
c	810	12.8	1.3	18	1	ABZ10527	Haematopoietic cel
c	811	12.8	1.3	18	1	ACD99918	Immunostimulatory
c	812	12.8	1.3	18	1	ACD99949	Immunostimulatory
c	813	12.8	1.3	18	1	ADA08050	DNA encoding human
c	814	12.8	1.3	18	1	ADB36975	Immunostimulatory
c	815	12.8	1.3	18	1	ADB36985	Immunostimulatory
c	816	12.8	1.3	18	1	ADB54055	Oligonucleotide 47
c	817	12.8	1.3	18	1	ADF17412	Nucleic acid assay
c	818	12.8	1.3	18	1	ABZ76994	Bovine DGAT PCR pr
c	819	12.8	1.3	18	1	ADK17529	Transposon plasmid
c	820	12.8	1.3	18	1	ADJ32230	Human PFM3a C box
c	821	12.8	1.3	18	1	ACA63217	Toll-like receptor
	822	12.8	1.3	18	1	ADK15543	Stromelysin promot
	823	12.8	1.3	18	1	ADM76163	NEPHA gene transcr
	824	12.8	1.3	18	1	ADQ93389	3-beta-hydroxyster
	825	12.8	1.3	18	1	ADQ93570	3-beta-hydroxyster
	826	12.8	1.3	18	1	ADT01342	Novel mutant prote
	827	12.6	1.3	13	1	ABH33279	Oligonucleotide SE
c	828	12.6	1.3	13	1	ABH33278	Oligonucleotide SE
c	829	12.6	1.3	15	1	AAX54839	C/EBP-beta antisen
c	830	12.6	1.3	15	1	AAA34286	Human adenosine re
c	831	12.6	1.3	15	1	AAF20408	Human C/EBP polynu
c	832	12.6	1.3	15	1	ABK81347	Human FOS gene all
c	833	12.6	1.3	15	1	ABZ96102	Human C/EBP antise
c	834	12.6	1.3	17	1	ABZ76684	Microtetraspora re
c	835	12.6	1.3	19	1	ABX13143	Rat p11 mutagenic
c	836	12.6	1.3	20	1	ADO52426	Human BRCA2 region

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 27, 2005, 16:55:02 ; Search time 8 Seconds
(without alignments)
3.429 Million cell updates/sec

Title: us-09-915-814-3
Perfect score: 970
Sequence: 1 cttcttgtaagagagtgcta.....tttctgagtgggtcgcagat 970

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 805 seqs, 14141 residues

Total number of hits satisfying chosen parameters: 1610

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 807 summaries

Database : rgedb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	18.2	1.9	24	1	E13893	ACCESSION:E13893
2	18.2	1.9	25	1	CQ627745	ACCESSION:CQ627745
3	18.2	1.9	25	1	CQ627746	ACCESSION:CQ627746
4	18.2	1.9	25	1	CQ627747	ACCESSION:CQ627747
5	18.2	1.9	25	1	AR468808	ACCESSION:AR468808
6	18.2	1.9	25	1	AR468809	ACCESSION:AR468809
7	18.2	1.9	25	1	AR468810	ACCESSION:AR468810
c 8	17.4	1.8	20	1	I25277	ACCESSION:I25277
9	17	1.8	20	1	AR292530	ACCESSION:AR292530
c 10	16.8	1.7	20	1	AX035665	ACCESSION:AX035665
c 11	16.8	1.7	22	1	AR233756	ACCESSION:AR233756
12	16.2	1.7	22	1	AX183869	ACCESSION:AX183869
13	16.2	1.7	22	1	AX591252	ACCESSION:AX591252
c 14	16.2	1.7	23	1	AX164418	ACCESSION:AX164418
15	15.6	1.6	22	1	A81881	ACCESSION:A81881
16	15.6	1.6	22	1	AR120684	ACCESSION:AR120684
17	15.6	1.6	22	1	BD135550	ACCESSION:BD135550
18	15.6	1.6	22	1	AR266660	ACCESSION:AR266660
19	15.4	1.6	17	1	CQ622852	ACCESSION:CQ622852
20	15.4	1.6	17	1	CQ622853	ACCESSION:CQ622853
21	15.4	1.6	17	1	AR463915	ACCESSION:AR463915
22	15.4	1.6	17	1	AR463916	ACCESSION:AR463916
c 23	15.4	1.6	17	1	AX532305	ACCESSION:AX532305
c 24	15.4	1.6	17	1	AX532307	ACCESSION:AX532307
25	15.4	1.6	17	1	AX672563	ACCESSION:AX672563
26	15.4	1.6	17	1	AX735475	ACCESSION:AX735475
c 27	15.4	1.6	20	1	E50955	ACCESSION:E50955
c 28	15.4	1.6	20	1	AX962802	ACCESSION:AX962802
29	15.4	1.6	22	1	AX360176	ACCESSION:AX360176
c 30	15.2	1.6	20	1	BD230194	ACCESSION:BD230194
31	15.2	1.6	20	1	BD232554	ACCESSION:BD232554
32	15.2	1.6	20	1	AR363588	ACCESSION:AR363588
33	15.2	1.6	20	1	AX009496	ACCESSION:AX009496
c 34	15.2	1.6	21	1	AR035033	ACCESSION:AR035033
c 35	15.2	1.6	21	1	BD276185	ACCESSION:BD276185
c 36	15.2	1.6	21	1	E11006	ACCESSION:E11006
37	15.2	1.6	21	1	I34868	ACCESSION:I34868
c 38	15.2	1.6	21	1	I88642	ACCESSION:I88642
c 39	15.2	1.6	21	1	AR264530	ACCESSION:AR264530
c 40	15	1.5	17	1	AX532306	ACCESSION:AX532306
41	15	1.5	18	1	BD191371	ACCESSION:BD191371
42	15	1.5	18	1	AR260472	ACCESSION:AR260472
43	15	1.5	18	1	BD085312	ACCESSION:BD085312
c 44	14.8	1.5	18	1	AR080724	ACCESSION:AR080724
c 45	14.8	1.5	18	1	AR162707	ACCESSION:AR162707
c 46	14.8	1.5	18	1	BD227767	ACCESSION:BD227767
47	14.8	1.5	18	1	AX659160	ACCESSION:AX659160
c 48	14.8	1.5	19	1	CQ801707	ACCESSION:CQ801707
c 49	14.8	1.5	19	1	CQ801828	ACCESSION:CQ801828
50	14.8	1.5	19	1	AR490936	ACCESSION:AR490936
c 51	14.8	1.5	19	1	AX659161	ACCESSION:AX659161
52	14.8	1.5	19	1	AX710207	ACCESSION:AX710207
53	14.8	1.5	20	1	AR067266	ACCESSION:AR067266
c 54	14.8	1.5	20	1	AR073718	ACCESSION:AR073718
55	14.8	1.5	20	1	AR136253	ACCESSION:AR136253
56	14.8	1.5	20	1	AR152732	ACCESSION:AR152732
c 57	14.8	1.5	20	1	AR152764	ACCESSION:AR152764
58	14.8	1.5	20	1	AR169283	ACCESSION:AR169283
c 59	14.8	1.5	20	1	AR169315	ACCESSION:AR169315
60	14.8	1.5	20	1	BD134188	ACCESSION:BD134188
c 61	14.8	1.5	20	1	BD134220	ACCESSION:BD134220
62	14.8	1.5	20	1	BD247708	ACCESSION:BD247708
63	14.8	1.5	20	1	AR252771	ACCESSION:AR252771
c 64	14.8	1.5	20	1	AR252791	ACCESSION:AR252791
65	14.8	1.5	20	1	AR255072	ACCESSION:AR255072
66	14.8	1.5	20	1	AR271128	ACCESSION:AR271128
67	14.8	1.5	20	1	AR337123	ACCESSION:AR337123
68	14.8	1.5	20	1	AR567361	ACCESSION:AR567361
c 69	14.8	1.5	20	1	AR567393	ACCESSION:AR567393
70	14.8	1.5	20	1	AR567540	ACCESSION:AR567540
71	14.8	1.5	20	1	AX139111	ACCESSION:AX139111
72	14.8	1.5	20	1	AX402356	ACCESSION:AX402356
73	14.8	1.5	20	1	BD014853	ACCESSION:BD014853
c 74	14.8	1.5	21	1	CQ830934	ACCESSION:CQ830934
75	14.4	1.5	16	1	BD087781	ACCESSION:BD087781
76	14.4	1.5	16	1	BD089447	ACCESSION:BD089447
77	14.4	1.5	16	1	AB068016	ACCESSION:AB068016
78	14.4	1.5	17	1	CQ622851	ACCESSION:CQ622851
79	14.4	1.5	17	1	CQ622854	ACCESSION:CQ622854
c 80	14.4	1.5	17	1	CQ622965	ACCESSION:CQ622965
c 81	14.4	1.5	17	1	CQ622966	ACCESSION:CQ622966
82	14.4	1.5	17	1	AR463914	ACCESSION:AR463914
83	14.4	1.5	17	1	AR463917	ACCESSION:AR463917
c 84	14.4	1.5	17	1	AR464028	ACCESSION:AR464028
c 85	14.4	1.5	17	1	AR464029	ACCESSION:AR464029
86	14.4	1.5	17	1	AX217683	ACCESSION:AX217683
c 87	14.4	1.5	17	1	AX227270	ACCESSION:AX227270
c 88	14.4	1.5	17	1	AX227405	ACCESSION:AX227405
c 89	14.4	1.5	17	1	AX532304	ACCESSION:AX532304
c 90	14.4	1.5	17	1	AX532308	ACCESSION:AX532308
91	14.4	1.5	17	1	AX672711	ACCESSION:AX672711
92	14.4	1.5	17	1	AX724315	ACCESSION:AX724315
c 93	14.4	1.5	17	1	AX756862	ACCESSION:AX756862
c 94	14.4	1.5	17	1	AX762013	ACCESSION:AX762013
95	14.4	1.5	19	1	AX129890	ACCESSION:AX129890
96	14.4	1.5	20	1	AR017550	ACCESSION:AR017550
97	14.4	1.5	20	1	CQ759163	ACCESSION:CQ759163
98	14.4	1.5	20	1	I21728	ACCESSION:I21728
99	14.4	1.5	20	1	I26109	ACCESSION:I26109
c 100	14.4	1.5	20	1	AR213522	ACCESSION:AR213522
101	14.4	1.5	20	1	AR255070	ACCESSION:AR255070
102	14.4	1.5	20	1	AR255071	ACCESSION:AR255071
103	14.4	1.5	20	1	AR255084	ACCESSION:AR255084
104	14.4	1.5	20	1	AR255085	ACCESSION:AR255085
c 105	14.4	1.5	20	1	AR315546	ACCESSION:AR315546
c 106	14.4	1.5	20	1	AR437316	ACCESSION:AR437316

c 107	14.4	1.5	20	1	AR442464	ACCESSION:AR442464
c 108	14.4	1.5	20	1	AX113639	ACCESSION:AX113639
c 109	14.4	1.5	20	1	AX708737	ACCESSION:AX708737
110	14.4	1.5	20	1	AX926057	ACCESSION:AX926057
111	14.4	1.5	20	1	AX926148	ACCESSION:AX926148
112	14.2	1.5	19	1	AR292785	ACCESSION:AR292785
113	14.2	1.5	19	1	AX018812	ACCESSION:AX018812
114	14.2	1.5	19	1	AX352913	ACCESSION:AX352913
115	14.2	1.5	19	1	AX362758	ACCESSION:AX362758
116	14.2	1.5	20	1	A41521	ACCESSION:A41521
117	14.2	1.5	20	1	A57905	ACCESSION:A57905
118	14.2	1.5	20	1	AR020468	ACCESSION:AR020468
c 119	14.2	1.5	20	1	AR158864	ACCESSION:AR158864
c 120	14.2	1.5	20	1	AR158865	ACCESSION:AR158865
121	14.2	1.5	20	1	BD137009	ACCESSION:BD137009
c 122	14.2	1.5	20	1	BD174239	ACCESSION:BD174239
c 123	14.2	1.5	20	1	BD174243	ACCESSION:BD174243
c 124	14.2	1.5	20	1	CQ764033	ACCESSION:CQ764033
c 125	14.2	1.5	20	1	CQ764166	ACCESSION:CQ764166
c 126	14.2	1.5	20	1	CQ764446	ACCESSION:CQ764446
c 127	14.2	1.5	20	1	CQ764501	ACCESSION:CQ764501
128	14.2	1.5	20	1	CQ767554	ACCESSION:CQ767554
129	14.2	1.5	20	1	CQ876529	ACCESSION:CQ876529
c 130	14.2	1.5	20	1	AR225992	ACCESSION:AR225992
c 131	14.2	1.5	20	1	AR235511	ACCESSION:AR235511
132	14.2	1.5	20	1	AR261622	ACCESSION:AR261622
133	14.2	1.5	20	1	AR303841	ACCESSION:AR303841
c 134	14.2	1.5	20	1	AR311976	ACCESSION:AR311976
c 135	14.2	1.5	20	1	AR312036	ACCESSION:AR312036
c 136	14.2	1.5	20	1	AR314198	ACCESSION:AR314198
137	14.2	1.5	20	1	AR314468	ACCESSION:AR314468
138	14.2	1.5	20	1	AR370194	ACCESSION:AR370194
c 139	14.2	1.5	20	1	AR371902	ACCESSION:AR371902
140	14.2	1.5	20	1	AX099758	ACCESSION:AX099758
141	14.2	1.5	20	1	AX134130	ACCESSION:AX134130
142	14.2	1.5	20	1	AX189739	ACCESSION:AX189739
143	14.2	1.5	20	1	AX292977	ACCESSION:AX292977
144	14.2	1.5	20	1	AX750451	ACCESSION:AX750451
c 145	14.2	1.5	20	1	AX766430	ACCESSION:AX766430
c 146	14.2	1.5	20	1	AX766434	ACCESSION:AX766434
147	14.2	1.5	20	1	AX955803	ACCESSION:AX955803
c 148	14.2	1.5	20	1	BD090075	ACCESSION:BD090075
c 149	14.2	1.5	20	1	AB068830	ACCESSION:AB068830
150	14	1.4	14	1	AR363099	ACCESSION:AR363099
151	14	1.4	17	1	CQ622849	ACCESSION:CQ622849
152	14	1.4	17	1	CQ622850	ACCESSION:CQ622850
c 153	14	1.4	17	1	CQ622963	ACCESSION:CQ622963
c 154	14	1.4	17	1	CQ622964	ACCESSION:CQ622964
155	14	1.4	17	1	AR463912	ACCESSION:AR463912
156	14	1.4	17	1	AR463913	ACCESSION:AR463913
c 157	14	1.4	17	1	AR464026	ACCESSION:AR464026
c 158	14	1.4	17	1	AR464027	ACCESSION:AR464027
159	14	1.4	17	1	AX725898	ACCESSION:AX725898
160	14	1.4	18	1	I92665	ACCESSION:I92665
c 161	14	1.4	20	1	AR100379	ACCESSION:AR100379
c 162	14	1.4	20	1	AR150034	ACCESSION:AR150034
c 163	14	1.4	20	1	BD227907	ACCESSION:BD227907
c 164	14	1.4	20	1	AR310832	ACCESSION:AR310832
165	13.8	1.4	17	1	BD241277	ACCESSION:BD241277
166	13.8	1.4	17	1	CQ615747	ACCESSION:CQ615747
167	13.8	1.4	17	1	CQ622847	ACCESSION:CQ622847
168	13.8	1.4	17	1	CQ622848	ACCESSION:CQ622848
c 169	13.8	1.4	17	1	CQ622967	ACCESSION:CQ622967
c 170	13.8	1.4	17	1	CQ622968	ACCESSION:CQ622968
c 171	13.8	1.4	17	1	AR196263	ACCESSION:AR196263
172	13.8	1.4	17	1	AR328770	ACCESSION:AR328770
173	13.8	1.4	17	1	AR456810	ACCESSION:AR456810
174	13.8	1.4	17	1	AR463910	ACCESSION:AR463910
175	13.8	1.4	17	1	AR463911	ACCESSION:AR463911
c 176	13.8	1.4	17	1	AR464030	ACCESSION:AR464030
c 177	13.8	1.4	17	1	AR464031	ACCESSION:AR464031
178	13.8	1.4	17	1	AR482778	ACCESSION:AR482778
179	13.8	1.4	17	1	AX218249	ACCESSION:AX218249
180	13.8	1.4	17	1	AX218250	ACCESSION:AX218250
181	13.8	1.4	17	1	AX272673	ACCESSION:AX272673
182	13.8	1.4	17	1	AX273198	ACCESSION:AX273198
183	13.8	1.4	17	1	AX475294	ACCESSION:AX475294
184	13.8	1.4	17	1	AX688306	ACCESSION:AX688306
185	13.8	1.4	17	1	AX688307	ACCESSION:AX688307
186	13.8	1.4	17	1	AX688308	ACCESSION:AX688308
c 187	13.8	1.4	17	1	AX710205	ACCESSION:AX710205
c 188	13.8	1.4	17	1	AX722998	ACCESSION:AX722998
189	13.8	1.4	17	1	AX723190	ACCESSION:AX723190
190	13.8	1.4	17	1	AX723403	ACCESSION:AX723403
c 191	13.8	1.4	17	1	AX724208	ACCESSION:AX724208
192	13.8	1.4	17	1	AX724823	ACCESSION:AX724823
193	13.8	1.4	17	1	AX730357	ACCESSION:AX730357
c 194	13.8	1.4	17	1	AX736285	ACCESSION:AX736285
195	13.8	1.4	17	1	AX736338	ACCESSION:AX736338
196	13.8	1.4	17	1	AX737511	ACCESSION:AX737511
197	13.8	1.4	17	1	AX757042	ACCESSION:AX757042
198	13.8	1.4	17	1	AX758322	ACCESSION:AX758322
c 199	13.8	1.4	18	1	A57744	ACCESSION:A57744
c 200	13.8	1.4	18	1	I62695	ACCESSION:I62695
201	13.8	1.4	18	1	AX705345	ACCESSION:AX705345
c 202	13.8	1.4	18	1	AX705346	ACCESSION:AX705346
c 203	13.8	1.4	18	1	AX838300	ACCESSION:AX838300
c 204	13.8	1.4	19	1	AR127420	ACCESSION:AR127420
c 205	13.8	1.4	19	1	BD195707	ACCESSION:BD195707
c 206	13.8	1.4	19	1	AR282800	ACCESSION:AR282800
c 207	13.8	1.4	19	1	AR300514	ACCESSION:AR300514
c 208	13.8	1.4	19	1	AR340596	ACCESSION:AR340596
209	13.8	1.4	19	1	AR490929	ACCESSION:AR490929
210	13.8	1.4	19	1	AR490949	ACCESSION:AR490949
211	13.8	1.4	19	1	AX129436	ACCESSION:AX129436
c 212	13.8	1.4	19	1	AX129940	ACCESSION:AX129940
213	13.8	1.4	19	1	AX130849	ACCESSION:AX130849
214	13.8	1.4	19	1	AX132384	ACCESSION:AX132384
c 215	13.4	1.4	15	1	BD266376	ACCESSION:BD266376
c 216	13.4	1.4	17	1	AR045661	ACCESSION:AR045661
217	13.4	1.4	17	1	CQ615745	ACCESSION:CQ615745
218	13.4	1.4	17	1	CQ615746	ACCESSION:CQ615746
219	13.4	1.4	17	1	CQ622855	ACCESSION:CQ622855
c 220	13.4	1.4	17	1	I52713	ACCESSION:I52713
221	13.4	1.4	17	1	AR192055	ACCESSION:AR192055
222	13.4	1.4	17	1	AR192218	ACCESSION:AR192218
223	13.4	1.4	17	1	AR192219	ACCESSION:AR192219
c 224	13.4	1.4	17	1	AR192582	ACCESSION:AR192582
225	13.4	1.4	17	1	AR211617	ACCESSION:AR211617
226	13.4	1.4	17	1	AR325937	ACCESSION:AR325937
227	13.4	1.4	17	1	AR326089	ACCESSION:AR326089
228	13.4	1.4	17	1	AR326090	ACCESSION:AR326090
c 229	13.4	1.4	17	1	AR326451	ACCESSION:AR326451
230	13.4	1.4	17	1	AR401932	ACCESSION:AR401932
231	13.4	1.4	17	1	AR456808	ACCESSION:AR456808
232	13.4	1.4	17	1	AR456809	ACCESSION:AR456809
233	13.4	1.4	17	1	AR463918	ACCESSION:AR463918
c 234	13.4	1.4	17	1	AX183741	ACCESSION:AX183741
235	13.4	1.4	17	1	AX218027	ACCESSION:AX218027
c 236	13.4	1.4	17	1	AX227269	ACCESSION:AX227269
237	13.4	1.4	17	1	AX475295	ACCESSION:AX475295
238	13.4	1.4	17	1	AX475296	ACCESSION:AX475296
c 239	13.4	1.4	17	1	AX532303	ACCESSION:AX532303
c 240	13.4	1.4	17	1	AX532309	ACCESSION:AX532309
241	13.4	1.4	17	1	AX672967	ACCESSION:AX672967
c 242	13.4	1.4	17	1	AX724133	ACCESSION:AX724133
c 243	13.4	1.4	17	1	AX724228	ACCESSION:AX724228
c 244	13.4	1.4	17	1	AX725569	ACCESSION:AX725569
245	13.4	1.4	17	1	AX731973	ACCESSION:AX731973
c 246	13.4	1.4	17	1	AX732048	ACCESSION:AX732048
247	13.4	1.4	17	1	AX733270	ACCESSION:AX733270
248	13.4	1.4	17	1	AX738184	ACCESSION:AX738184
249	13.4	1.4	17	1	AX757681	ACCESSION:AX757681
c 250	13.4	1.4	17	1	AX758075	ACCESSION:AX758075
251	13.4	1.4	17	1	AX760231	ACCESSION:AX760231
c 252	13.4	1.4	17	1	AX761573	ACCESSION:AX761573

	253	13.4	1.4	17	1	BD067432	ACCESSION:BD067432
	254	13.4	1.4	18	1	I77229	ACCESSION:I77229
	255	13.4	1.4	18	1	AR295621	ACCESSION:AR295621
c	256	13.4	1.4	18	1	AR297751	ACCESSION:AR297751
	257	13.4	1.4	18	1	AX837998	ACCESSION:AX837998
	258	13.4	1.4	18	1	AX838137	ACCESSION:AX838137
	259	13.4	1.4	19	1	AR004645	ACCESSION:AR004645
	260	13.4	1.4	19	1	AR034557	ACCESSION:AR034557
	261	13.4	1.4	19	1	I89247	ACCESSION:I89247
	262	13.4	1.4	19	1	AR364420	ACCESSION:AR364420
c	263	13.4	1.4	19	1	AX115354	ACCESSION:AX115354
c	264	13.4	1.4	19	1	AX128802	ACCESSION:AX128802
	265	13.4	1.4	19	1	AX134135	ACCESSION:AX134135
	266	13.4	1.4	19	1	AX189744	ACCESSION:AX189744
	267	13.4	1.4	19	1	AX615126	ACCESSION:AX615126
c	268	13.2	1.4	18	1	A66926	ACCESSION:A66926
	269	13.2	1.4	18	1	A89440	ACCESSION:A89440
c	270	13.2	1.4	18	1	AR042353	ACCESSION:AR042353
	271	13.2	1.4	18	1	AR068299	ACCESSION:AR068299
c	272	13.2	1.4	18	1	AR096626	ACCESSION:AR096626
	273	13.2	1.4	18	1	AR098794	ACCESSION:AR098794
	274	13.2	1.4	18	1	AR130025	ACCESSION:AR130025
	275	13.2	1.4	18	1	BD185912	ACCESSION:BD185912
c	276	13.2	1.4	18	1	BD185921	ACCESSION:BD185921
	277	13.2	1.4	18	1	BD250587	ACCESSION:BD250587
c	278	13.2	1.4	18	1	I68997	ACCESSION:I68997
	279	13.2	1.4	18	1	I72012	ACCESSION:I72012
	280	13.2	1.4	18	1	I75091	ACCESSION:I75091
	281	13.2	1.4	18	1	AR211740	ACCESSION:AR211740
	282	13.2	1.4	18	1	AR215589	ACCESSION:AR215589
c	283	13.2	1.4	18	1	AR232057	ACCESSION:AR232057
c	284	13.2	1.4	18	1	AR253595	ACCESSION:AR253595
	285	13.2	1.4	18	1	AR281361	ACCESSION:AR281361
c	286	13.2	1.4	18	1	AR294630	ACCESSION:AR294630
c	287	13.2	1.4	18	1	AR364838	ACCESSION:AR364838
c	288	13.2	1.4	18	1	AR488428	ACCESSION:AR488428
c	289	13.2	1.4	18	1	AX179590	ACCESSION:AX179590
c	290	13.2	1.4	18	1	AX637798	ACCESSION:AX637798
c	291	13.2	1.4	18	1	AX696650	ACCESSION:AX696650
	292	13.2	1.4	18	1	AX763946	ACCESSION:AX763946
	293	13.2	1.4	18	1	BD066953	ACCESSION:BD066953
	294	13.2	1.4	18	1	BD085546	ACCESSION:BD085546
	295	13.2	1.4	18	1	BD103977	ACCESSION:BD103977
	296	13.2	1.4	18	1	HSY13354	ACCESSION:Y13354
c	297	13	1.3	13	1	E32325	ACCESSION:E32325
c	298	13	1.3	16	1	CQ808624	ACCESSION:CQ808624
c	299	13	1.3	16	1	AR305474	ACCESSION:AR305474
c	300	13	1.3	16	1	AR309578	ACCESSION:AR309578
c	301	13	1.3	16	1	BD106385	ACCESSION:BD106385
c	302	13	1.3	17	1	AR045663	ACCESSION:AR045663
c	303	13	1.3	17	1	AR046710	ACCESSION:AR046710
c	304	13	1.3	17	1	AR046712	ACCESSION:AR046712
c	305	13	1.3	17	1	BD241434	ACCESSION:BD241434
c	306	13	1.3	17	1	CQ622962	ACCESSION:CQ622962
c	307	13	1.3	17	1	I52715	ACCESSION:I52715
c	308	13	1.3	17	1	I53762	ACCESSION:I53762
c	309	13	1.3	17	1	I53764	ACCESSION:I53764
c	310	13	1.3	17	1	I57962	ACCESSION:I57962
c	311	13	1.3	17	1	AR464025	ACCESSION:AR464025
c	312	13	1.3	17	1	AR482935	ACCESSION:AR482935
c	313	13	1.3	17	1	AX226910	ACCESSION:AX226910
c	314	13	1.3	17	1	AX226911	ACCESSION:AX226911
c	315	13	1.3	17	1	AX590783	ACCESSION:AX590783
c	316	13	1.3	17	1	AX732310	ACCESSION:AX732310
	317	13	1.3	17	1	AX733777	ACCESSION:AX733777
c	318	13	1.3	17	1	AX735062	ACCESSION:AX735062
c	319	13	1.3	17	1	AX759640	ACCESSION:AX759640
	320	13	1.3	17	1	AX762964	ACCESSION:AX762964
	321	13	1.3	18	1	AX777824	ACCESSION:AX777824
	322	13	1.3	18	1	BD104973	ACCESSION:BD104973
	323	12.8	1.3	16	1	A21773	ACCESSION:A21773
c	324	12.8	1.3	16	1	CQ857871	ACCESSION:CQ857871
	325	12.8	1.3	16	1	CQ858610	ACCESSION:CQ858610
c	326	12.8	1.3	16	1	AX247596	ACCESSION:AX247596
	327	12.8	1.3	17	1	A97970	ACCESSION:A97970
	328	12.8	1.3	17	1	AR039283	ACCESSION:AR039283
c	329	12.8	1.3	17	1	AR130717	ACCESSION:AR130717
	330	12.8	1.3	17	1	BD254150	ACCESSION:BD254150
	331	12.8	1.3	17	1	BD254847	ACCESSION:BD254847
c	332	12.8	1.3	17	1	BD255278	ACCESSION:BD255278
c	333	12.8	1.3	17	1	BD255279	ACCESSION:BD255279
	334	12.8	1.3	17	1	BD259218	ACCESSION:BD259218
c	335	12.8	1.3	17	1	BD259317	ACCESSION:BD259317
	336	12.8	1.3	17	1	CQ615748	ACCESSION:CQ615748
	337	12.8	1.3	17	1	CQ622846	ACCESSION:CQ622846
c	338	12.8	1.3	17	1	CQ622969	ACCESSION:CQ622969
c	339	12.8	1.3	17	1	AR192393	ACCESSION:AR192393
c	340	12.8	1.3	17	1	AR196262	ACCESSION:AR196262
	341	12.8	1.3	17	1	AR254963	ACCESSION:AR254963
	342	12.8	1.3	17	1	AR286197	ACCESSION:AR286197
c	343	12.8	1.3	17	1	AR326262	ACCESSION:AR326262
c	344	12.8	1.3	17	1	AR370341	ACCESSION:AR370341
	345	12.8	1.3	17	1	AR398187	ACCESSION:AR398187
	346	12.8	1.3	17	1	AR456811	ACCESSION:AR456811
	347	12.8	1.3	17	1	AR463909	ACCESSION:AR463909
c	348	12.8	1.3	17	1	AR464032	ACCESSION:AR464032
c	349	12.8	1.3	17	1	AR534772	ACCESSION:AR534772
	350	12.8	1.3	17	1	AX218251	ACCESSION:AX218251
c	351	12.8	1.3	17	1	AX263928	ACCESSION:AX263928
	352	12.8	1.3	17	1	AX263929	ACCESSION:AX263929
	353	12.8	1.3	17	1	AX272672	ACCESSION:AX272672
	354	12.8	1.3	17	1	AX272887	ACCESSION:AX272887
c	355	12.8	1.3	17	1	AX273134	ACCESSION:AX273134
	356	12.8	1.3	17	1	AX273157	ACCESSION:AX273157
	357	12.8	1.3	17	1	AX273199	ACCESSION:AX273199
c	358	12.8	1.3	17	1	AX273264	ACCESSION:AX273264
	359	12.8	1.3	17	1	AX393393	ACCESSION:AX393393
	360	12.8	1.3	17	1	AX393394	ACCESSION:AX393394
c	361	12.8	1.3	17	1	AX421804	ACCESSION:AX421804
c	362	12.8	1.3	17	1	AX421805	ACCESSION:AX421805
c	363	12.8	1.3	17	1	AX423197	ACCESSION:AX423197
c	364	12.8	1.3	17	1	AX423758	ACCESSION:AX423758
	365	12.8	1.3	17	1	AX428848	ACCESSION:AX428848
	366	12.8	1.3	17	1	AX475293	ACCESSION:AX475293
c	367	12.8	1.3	17	1	AX578684	ACCESSION:AX578684
c	368	12.8	1.3	17	1	AX578685	ACCESSION:AX578685
	369	12.8	1.3	17	1	AX578913	ACCESSION:AX578913
c	370	12.8	1.3	17	1	AX648380	ACCESSION:AX648380
c	371	12.8	1.3	17	1	AX648381	ACCESSION:AX648381
	372	12.8	1.3	17	1	AX672679	ACCESSION:AX672679
	373	12.8	1.3	17	1	AX672919	ACCESSION:AX672919
	374	12.8	1.3	17	1	AX673352	ACCESSION:AX673352
	375	12.8	1.3	17	1	AX688305	ACCESSION:AX688305
	376	12.8	1.3	17	1	AX688309	ACCESSION:AX688309
	377	12.8	1.3	17	1	AX690769	ACCESSION:AX690769
	378	12.8	1.3	17	1	AX690770	ACCESSION:AX690770
	379	12.8	1.3	17	1	AX693583	ACCESSION:AX693583
	380	12.8	1.3	17	1	AX693584	ACCESSION:AX693584
c	381	12.8	1.3	17	1	AX699223	ACCESSION:AX699223
	382	12.8	1.3	17	1	AX722984	ACCESSION:AX722984
c	383	12.8	1.3	17	1	AX722996	ACCESSION:AX722996
c	384	12.8	1.3	17	1	AX723002	ACCESSION:AX723002
	385	12.8	1.3	17	1	AX723794	ACCESSION:AX723794
c	386	12.8	1.3	17	1	AX723959	ACCESSION:AX723959
	387	12.8	1.3	17	1	AX725865	ACCESSION:AX725865
c	388	12.8	1.3	17	1	AX727279	ACCESSION:AX727279
c	389	12.8	1.3	17	1	AX729573	ACCESSION:AX729573
	390	12.8	1.3	17	1	AX730751	ACCESSION:AX730751
	391	12.8	1.3	17	1	AX736827	ACCESSION:AX736827
	392	12.8	1.3	17	1	AX737152	ACCESSION:AX737152
	393	12.8	1.3	17	1	AX739018	ACCESSION:AX739018
c	394	12.8	1.3	17	1	AX758417	ACCESSION:AX758417
	395	12.8	1.3	17	1	AX759195	ACCESSION:AX759195
	396	12.8	1.3	17	1	AX759711	ACCESSION:AX759711
	397	12.8	1.3	17	1	AX761423	ACCESSION:AX761423
c	398	12.8	1.3	17	1	AX761783	ACCESSION:AX761783

c 399	12.8	1.3	17	1	AX762542	ACCESSION:AX762542
c 400	12.8	1.3	17	1	AX783962	ACCESSION:AX783962
c 401	12.8	1.3	17	1	AX783963	ACCESSION:AX783963
c 402	12.8	1.3	17	1	BD105092	ACCESSION:BD105092
403	12.8	1.3	18	1	AR054591	ACCESSION:AR054591
c 404	12.8	1.3	18	1	AR066819	ACCESSION:AR066819
c 405	12.8	1.3	18	1	AR098792	ACCESSION:AR098792
c 406	12.8	1.3	18	1	BD235033	ACCESSION:BD235033
407	12.8	1.3	18	1	AR292331	ACCESSION:AR292331
c 408	12.8	1.3	18	1	AR351484	ACCESSION:AR351484
409	12.8	1.3	18	1	AR353630	ACCESSION:AR353630
410	12.8	1.3	18	1	AR481871	ACCESSION:AR481871
c 411	12.8	1.3	18	1	AX009104	ACCESSION:AX009104
c 412	12.8	1.3	18	1	AX104436	ACCESSION:AX104436
c 413	12.8	1.3	18	1	AX104470	ACCESSION:AX104470
c 414	12.8	1.3	18	1	AX355440	ACCESSION:AX355440
c 415	12.8	1.3	18	1	AX355441	ACCESSION:AX355441
416	12.8	1.3	18	1	AX412171	ACCESSION:AX412171
c 417	12.8	1.3	18	1	AX547489	ACCESSION:AX547489
c 418	12.8	1.3	18	1	AX547523	ACCESSION:AX547523
c 419	12.8	1.3	18	1	AX599327	ACCESSION:AX599327
420	12.8	1.3	18	1	AX661825	ACCESSION:AX661825
c 421	12.8	1.3	18	1	AX708197	ACCESSION:AX708197
c 422	12.8	1.3	18	1	AX822219	ACCESSION:AX822219
c 423	12.8	1.3	18	1	AX825859	ACCESSION:AX825859
c 424	12.6	1.3	17	1	BD186577	ACCESSION:BD186577
c 425	12.6	1.3	19	1	AX710207	ACCESSION:AX710207
c 426	12.4	1.3	14	1	AR067994	ACCESSION:AR067994
c 427	12.4	1.3	14	1	BD233321	ACCESSION:BD233321
c 428	12.4	1.3	14	1	AR300207	ACCESSION:AR300207
429	12.4	1.3	14	1	AR407917	ACCESSION:AR407917
c 430	12.4	1.3	14	1	AX007875	ACCESSION:AX007875
c 431	12.4	1.3	15	1	A35569	ACCESSION:A35569
c 432	12.4	1.3	15	1	AR056415	ACCESSION:AR056415
c 433	12.4	1.3	15	1	AR114173	ACCESSION:AR114173
c 434	12.4	1.3	15	1	BD233337	ACCESSION:BD233337
c 435	12.4	1.3	15	1	BD251057	ACCESSION:BD251057
c 436	12.4	1.3	15	1	AR409497	ACCESSION:AR409497
c 437	12.4	1.3	15	1	AX007891	ACCESSION:AX007891
c 438	12.4	1.3	15	1	AX633321	ACCESSION:AX633321
c 439	12.4	1.3	16	1	AR211597	ACCESSION:AR211597
c 440	12.4	1.3	16	1	AR328443	ACCESSION:AR328443
c 441	12.4	1.3	16	1	AR436192	ACCESSION:AR436192
442	12.4	1.3	16	1	AX419963	ACCESSION:AX419963
c 443	12.4	1.3	17	1	A58019	ACCESSION:A58019
444	12.4	1.3	17	1	AR014263	ACCESSION:AR014263
c 445	12.4	1.3	17	1	AR040297	ACCESSION:AR040297
c 446	12.4	1.3	17	1	AR046854	ACCESSION:AR046854
447	12.4	1.3	17	1	AR057466	ACCESSION:AR057466
c 448	12.4	1.3	17	1	AR057512	ACCESSION:AR057512
c 449	12.4	1.3	17	1	AR057728	ACCESSION:AR057728
450	12.4	1.3	17	1	AR057770	ACCESSION:AR057770
c 451	12.4	1.3	17	1	AR057789	ACCESSION:AR057789
c 452	12.4	1.3	17	1	AR057790	ACCESSION:AR057790
453	12.4	1.3	17	1	AR065790	ACCESSION:AR065790
454	12.4	1.3	17	1	AR115224	ACCESSION:AR115224
c 455	12.4	1.3	17	1	AR115270	ACCESSION:AR115270
c 456	12.4	1.3	17	1	AR115486	ACCESSION:AR115486
457	12.4	1.3	17	1	AR115528	ACCESSION:AR115528
c 458	12.4	1.3	17	1	AR115547	ACCESSION:AR115547
c 459	12.4	1.3	17	1	AR115548	ACCESSION:AR115548
460	12.4	1.3	17	1	BD139921	ACCESSION:BD139921
461	12.4	1.3	17	1	BD203414	ACCESSION:BD203414
462	12.4	1.3	17	1	BD241324	ACCESSION:BD241324
463	12.4	1.3	17	1	BD259173	ACCESSION:BD259173
464	12.4	1.3	17	1	CQ615744	ACCESSION:CQ615744
465	12.4	1.3	17	1	CQ622856	ACCESSION:CQ622856
c 466	12.4	1.3	17	1	CQ623573	ACCESSION:CQ623573
c 467	12.4	1.3	17	1	CQ623574	ACCESSION:CQ623574
c 468	12.4	1.3	17	1	CQ623575	ACCESSION:CQ623575
c 469	12.4	1.3	17	1	CQ623576	ACCESSION:CQ623576
c 470	12.4	1.3	17	1	I53906	ACCESSION:I53906
471	12.4	1.3	17	1	I73170	ACCESSION:I73170
472	12.4	1.3	17	1	AR186361	ACCESSION:AR186361
c 473	12.4	1.3	17	1	AR190365	ACCESSION:AR190365
c 474	12.4	1.3	17	1	AR190366	ACCESSION:AR190366
475	12.4	1.3	17	1	AR286006	ACCESSION:AR286006
476	12.4	1.3	17	1	AR302289	ACCESSION:AR302289
477	12.4	1.3	17	1	AR322992	ACCESSION:AR322992
c 478	12.4	1.3	17	1	AR325310	ACCESSION:AR325310
c 479	12.4	1.3	17	1	AR325311	ACCESSION:AR325311
480	12.4	1.3	17	1	AR397996	ACCESSION:AR397996
c 481	12.4	1.3	17	1	AR402479	ACCESSION:AR402479
c 482	12.4	1.3	17	1	AR434349	ACCESSION:AR434349
c 483	12.4	1.3	17	1	AR434350	ACCESSION:AR434350
c 484	12.4	1.3	17	1	AR434351	ACCESSION:AR434351
c 485	12.4	1.3	17	1	AR434352	ACCESSION:AR434352
c 486	12.4	1.3	17	1	AR434440	ACCESSION:AR434440
c 487	12.4	1.3	17	1	AR434441	ACCESSION:AR434441
c 488	12.4	1.3	17	1	AR434442	ACCESSION:AR434442
c 489	12.4	1.3	17	1	AR434443	ACCESSION:AR434443
490	12.4	1.3	17	1	AR456807	ACCESSION:AR456807
491	12.4	1.3	17	1	AR463919	ACCESSION:AR463919
c 492	12.4	1.3	17	1	AR464636	ACCESSION:AR464636
c 493	12.4	1.3	17	1	AR464637	ACCESSION:AR464637
c 494	12.4	1.3	17	1	AR464638	ACCESSION:AR464638
c 495	12.4	1.3	17	1	AR464639	ACCESSION:AR464639
496	12.4	1.3	17	1	AR482825	ACCESSION:AR482825
c 497	12.4	1.3	17	1	AX139251	ACCESSION:AX139251
498	12.4	1.3	17	1	AX217682	ACCESSION:AX217682
499	12.4	1.3	17	1	AX218125	ACCESSION:AX218125
c 500	12.4	1.3	17	1	AX226816	ACCESSION:AX226816
c 501	12.4	1.3	17	1	AX227181	ACCESSION:AX227181
c 502	12.4	1.3	17	1	AX227182	ACCESSION:AX227182
c 503	12.4	1.3	17	1	AX227183	ACCESSION:AX227183
c 504	12.4	1.3	17	1	AX263072	ACCESSION:AX263072
505	12.4	1.3	17	1	AX263073	ACCESSION:AX263073
506	12.4	1.3	17	1	AX475297	ACCESSION:AX475297
c 507	12.4	1.3	17	1	AX527151	ACCESSION:AX527151
c 508	12.4	1.3	17	1	AX527152	ACCESSION:AX527152
c 509	12.4	1.3	17	1	AX527153	ACCESSION:AX527153
c 510	12.4	1.3	17	1	AX527154	ACCESSION:AX527154
c 511	12.4	1.3	17	1	AX532302	ACCESSION:AX532302
c 512	12.4	1.3	17	1	AX532310	ACCESSION:AX532310
513	12.4	1.3	17	1	AX578912	ACCESSION:AX578912
514	12.4	1.3	17	1	AX579853	ACCESSION:AX579853
515	12.4	1.3	17	1	AX634562	ACCESSION:AX634562
c 516	12.4	1.3	17	1	AX634572	ACCESSION:AX634572
517	12.4	1.3	17	1	AX634795	ACCESSION:AX634795
c 518	12.4	1.3	17	1	AX634808	ACCESSION:AX634808
c 519	12.4	1.3	17	1	AX634833	ACCESSION:AX634833
c 520	12.4	1.3	17	1	AX634835	ACCESSION:AX634835
c 521	12.4	1.3	17	1	AX648382	ACCESSION:AX648382
c 522	12.4	1.3	17	1	AX648383	ACCESSION:AX648383
523	12.4	1.3	17	1	AX671885	ACCESSION:AX671885
c 524	12.4	1.3	17	1	AX673535	ACCESSION:AX673535
525	12.4	1.3	17	1	AX673690	ACCESSION:AX673690
526	12.4	1.3	17	1	AX688303	ACCESSION:AX688303
527	12.4	1.3	17	1	AX688304	ACCESSION:AX688304
c 528	12.4	1.3	17	1	AX688466	ACCESSION:AX688466
c 529	12.4	1.3	17	1	AX688467	ACCESSION:AX688467
c 530	12.4	1.3	17	1	AX688468	ACCESSION:AX688468
c 531	12.4	1.3	17	1	AX688469	ACCESSION:AX688469
532	12.4	1.3	17	1	AX723094	ACCESSION:AX723094
533	12.4	1.3	17	1	AX724140	ACCESSION:AX724140
534	12.4	1.3	17	1	AX724916	ACCESSION:AX724916
c 535	12.4	1.3	17	1	AX725258	ACCESSION:AX725258
536	12.4	1.3	17	1	AX725790	ACCESSION:AX725790
c 537	12.4	1.3	17	1	AX726362	ACCESSION:AX726362
c 538	12.4	1.3	17	1	AX727345	ACCESSION:AX727345
c 539	12.4	1.3	17	1	AX728438	ACCESSION:AX728438
540	12.4	1.3	17	1	AX729385	ACCESSION:AX729385
c 541	12.4	1.3	17	1	AX729677	ACCESSION:AX729677
542	12.4	1.3	17	1	AX729729	ACCESSION:AX729729
c 543	12.4	1.3	17	1	AX730652	ACCESSION:AX730652
544	12.4	1.3	17	1	AX731932	ACCESSION:AX731932

	545	12.4	1.3	17	1	AX732254	ACCESSION:AX732254
	546	12.4	1.3	17	1	AX733857	ACCESSION:AX733857
c	547	12.4	1.3	17	1	AX735317	ACCESSION:AX735317
	548	12.4	1.3	17	1	AX735539	ACCESSION:AX735539
	549	12.4	1.3	17	1	AX736300	ACCESSION:AX736300
	550	12.4	1.3	17	1	AX736313	ACCESSION:AX736313
	551	12.4	1.3	17	1	AX738273	ACCESSION:AX738273
	552	12.4	1.3	17	1	AX739003	ACCESSION:AX739003
	553	12.4	1.3	17	1	AX739342	ACCESSION:AX739342
	554	12.4	1.3	17	1	AX739832	ACCESSION:AX739832
	555	12.4	1.3	17	1	AX756942	ACCESSION:AX756942
c	556	12.4	1.3	17	1	AX758728	ACCESSION:AX758728
	557	12.4	1.3	17	1	AX759153	ACCESSION:AX759153
	558	12.4	1.3	17	1	AX759540	ACCESSION:AX759540
c	559	12.4	1.3	17	1	AX760640	ACCESSION:AX760640
	560	12.4	1.3	17	1	AX762440	ACCESSION:AX762440
c	561	12.4	1.3	17	1	BD013535	ACCESSION:BD013535
c	562	12.4	1.3	17	1	BD067979	ACCESSION:BD067979
	563	12.2	1.3	17	1	AX726362	ACCESSION:AX726362
c	564	12.2	1.3	17	1	A04032	ACCESSION:A04032
c	565	12.2	1.3	17	1	A07276	ACCESSION:A07276
c	566	12.2	1.3	17	1	A14911	ACCESSION:A14911
c	567	12.2	1.3	17	1	A30566	ACCESSION:A30566
c	568	12.2	1.3	17	1	A34171	ACCESSION:A34171
c	569	12.2	1.3	17	1	A34558	ACCESSION:A34558
c	570	12.2	1.3	17	1	A66925	ACCESSION:A66925
c	571	12.2	1.3	17	1	A75920	ACCESSION:A75920
	572	12.2	1.3	17	1	AR029643	ACCESSION:AR029643
	573	12.2	1.3	17	1	AR040155	ACCESSION:AR040155
c	574	12.2	1.3	17	1	AR045937	ACCESSION:AR045937
c	575	12.2	1.3	17	1	AR046572	ACCESSION:AR046572
c	576	12.2	1.3	17	1	AR048978	ACCESSION:AR048978
c	577	12.2	1.3	17	1	AR064279	ACCESSION:AR064279
	578	12.2	1.3	17	1	AR124366	ACCESSION:AR124366
	579	12.2	1.3	17	1	AR157378	ACCESSION:AR157378
c	580	12.2	1.3	17	1	AR164672	ACCESSION:AR164672
c	581	12.2	1.3	17	1	BD187272	ACCESSION:BD187272
c	582	12.2	1.3	17	1	BD200793	ACCESSION:BD200793
c	583	12.2	1.3	17	1	BD200794	ACCESSION:BD200794
c	584	12.2	1.3	17	1	BD203227	ACCESSION:BD203227
c	585	12.2	1.3	17	1	BD203339	ACCESSION:BD203339
c	586	12.2	1.3	17	1	BD241216	ACCESSION:BD241216
	587	12.2	1.3	17	1	BD241276	ACCESSION:BD241276
c	588	12.2	1.3	17	1	BD241679	ACCESSION:BD241679
	589	12.2	1.3	17	1	BD241716	ACCESSION:BD241716
c	590	12.2	1.3	17	1	BD253930	ACCESSION:BD253930
c	591	12.2	1.3	17	1	BD253981	ACCESSION:BD253981
	592	12.2	1.3	17	1	BD254446	ACCESSION:BD254446
c	593	12.2	1.3	17	1	BD254701	ACCESSION:BD254701
	594	12.2	1.3	17	1	BD255102	ACCESSION:BD255102
c	595	12.2	1.3	17	1	BD255280	ACCESSION:BD255280
c	596	12.2	1.3	17	1	BD255281	ACCESSION:BD255281
c	597	12.2	1.3	17	1	BD258334	ACCESSION:BD258334
c	598	12.2	1.3	17	1	BD259500	ACCESSION:BD259500
	599	12.2	1.3	17	1	BD259634	ACCESSION:BD259634
	600	12.2	1.3	17	1	CQ615384	ACCESSION:CQ615384
	601	12.2	1.3	17	1	CQ615505	ACCESSION:CQ615505
	602	12.2	1.3	17	1	CQ615655	ACCESSION:CQ615655
	603	12.2	1.3	17	1	CQ615709	ACCESSION:CQ615709
	604	12.2	1.3	17	1	CQ615710	ACCESSION:CQ615710
	605	12.2	1.3	17	1	CQ615969	ACCESSION:CQ615969
c	606	12.2	1.3	17	1	CQ616325	ACCESSION:CQ616325
c	607	12.2	1.3	17	1	CQ616588	ACCESSION:CQ616588
c	608	12.2	1.3	17	1	CQ616830	ACCESSION:CQ616830
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c	613	12.2	1.3	17	1	CQ621833	ACCESSION:CQ621833
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	616	12.2	1.3	17	1	CQ623922	ACCESSION:CQ623922
	617	12.2	1.3	17	1	CQ623923	ACCESSION:CQ623923
	618	12.2	1.3	17	1	CQ623925	ACCESSION:CQ623925
	619	12.2	1.3	17	1	CQ774981	ACCESSION:CQ774981
	620	12.2	1.3	17	1	CQ779653	ACCESSION:CQ779653
	621	12.2	1.3	17	1	I27377	ACCESSION:I27377
	622	12.2	1.3	17	1	I34602	ACCESSION:I34602
	623	12.2	1.3	17	1	I37605	ACCESSION:I37605
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	626	12.2	1.3	17	1	I94455	ACCESSION:I94455
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	628	12.2	1.3	17	1	AR189898	ACCESSION:AR189898
c	629	12.2	1.3	17	1	AR190517	ACCESSION:AR190517
	630	12.2	1.3	17	1	AR192027	ACCESSION:AR192027
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	635	12.2	1.3	17	1	AR286098	ACCESSION:AR286098
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	637	12.2	1.3	17	1	AR286429	ACCESSION:AR286429
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	675	12.2	1.3	17	1	AR464986	ACCESSION:AR464986
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	680	12.2	1.3	17	1	AR483217	ACCESSION:AR483217
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	682	12.2	1.3	17	1	AX214877	ACCESSION:AX214877
	683	12.2	1.3	17	1	AX215602	ACCESSION:AX215602
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700	12.2	1.3	17	1	AX325650	ACCESSION:AX325650
701	12.2	1.3	17	1	AX402539	ACCESSION:AX402539
c 702	12.2	1.3	17	1	AX422574	ACCESSION:AX422574
c 703	12.2	1.3	17	1	AX422575	ACCESSION:AX422575
c 704	12.2	1.3	17	1	AX422577	ACCESSION:AX422577
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c 719	12.2	1.3	17	1	AX671928	ACCESSION:AX671928
720	12.2	1.3	17	1	AX672019	ACCESSION:AX672019
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722	12.2	1.3	17	1	AX672509	ACCESSION:AX672509
c 723	12.2	1.3	17	1	AX672617	ACCESSION:AX672617
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c 764	12.2	1.3	17	1	AX733855	ACCESSION:AX733855
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786	12.2	1.3	17	1	AX759565	ACCESSION:AX759565
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807	12.2	1.3	17	1	MUSIGDJAK	ACCESSION:L36733

ALIGNMENTS

RESULT 1
E13893/c
LOCUS E13893 24 bp DNA linear PAT 27-APR-1998
DEFINITION PCR primer for gaining human G protein-coupling receptor gene.
ACCESSION E13893
VERSION E13893.1 GI:3252660
KEYWORDS JP 1997238686-A/2.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 24)
AUTHORS Hinuma,K. and Fujii,A.
TITLE NEW G-PROTEIN CONJUGATED TYPE RECEPTOR PROTEIN, ITS PRODUCTION AND
JOURNAL Patent: JP 1997238686-A 2 16-SEP-1997;
TAKEDA CHEM IND LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1997238686-A/2
PD 16-SEP-1997
PF 07-MAR-1996 JP 1996050678
PI HINUMA KUNIJI, FUJII AKIRA
PC C12N15/09,A61K48/00,C07H21/04,C12N1/21,C12P21/02,C12P21/08, PC
C12Q1/02,
PC G01N33/566//A61K39/395,(C12N1/21,C12R1:19),(C12P21/02, PC

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;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1369
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1369

  Query Match             1.4%;  Score 14;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+02;
  Matches   14;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        436 AAACCAAAGACCCC 449
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Db         18 AAACCAAAGACCCC 5


RESULT 99
US-08-679-645-728/c
; Sequence 728, Application US/08679645
; Patent No. 6350934
;  GENERAL INFORMATION:
;    APPLICANT:  Zwick, Michael G.
;    APPLICANT:  Edington, Brent E.
;    APPLICANT:  McSwiggen, James A.
;    APPLICANT:  Merlo, Patricia Ann Owens
;    APPLICANT:  Guo, Lining
;    APPLICANT:  Skokut, Thomas A.
;    APPLICANT:  Young, Scott A.
;    APPLICANT:  Folkerts, Otto
;    APPLICANT:  Merlo, Donald J.
;    TITLE OF INVENTION:  COMPOSITION AND METHODS FOR
;    TITLE OF INVENTION:  MODULATION OF GENE EXPRESSION
;    TITLE OF INVENTION:  IN PLANTS
;    NUMBER OF SEQUENCES:  1263
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/679,645
;      FILING DATE:  July 12, 1996
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/001,135
;      FILING DATE:  July 13, 1995
;      APPLICATION NUMBER:  08/300,726
;      FILING DATE:  September 2, 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  219/247
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  728:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-679-645-728

  Query Match             1.4%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db         17 CTCCCACCAAACAAACA 1


RESULT 100
US-09-371-772B-6172
; Sequence 6172, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6172
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-6172

  Query Match             1.4%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 1.1e+02;
  Matches   13;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 GAAAUGACACUGGAGCC 17


RESULT 101
US-09-866-108A-487
; Sequence 487, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
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;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 487
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-487

  Query Match             1.4%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        699 CTGGGCCAGGAGAGCCA 715
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RESULT 102
US-09-866-108A-7587
; Sequence 7587, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7587
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-7587

  Query Match             1.4%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Db          1 AACTGAAGAGGAAGTGC 17


RESULT 103
US-09-866-108A-7588
; Sequence 7588, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
;  APPLICANT:  RANK, David R.
;  APPLICANT:  CHEN, Wensheng
;  APPLICANT:  SHANNON, Mark
;  TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
;  FILE REFERENCE: AEOMICA-7
;  CURRENT APPLICATION NUMBER: US/09/866,108A
;  CURRENT FILING DATE:  2001-05-25
;  PRIOR APPLICATION NUMBER: US 60/207,456
;  PRIOR FILING DATE: 2000-05-26
;  PRIOR APPLICATION NUMBER: GB 24263.6
;  PRIOR FILING DATE: 2000-10-04
;  PRIOR APPLICATION NUMBER: US 60/236,359
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: PCT/US01/00666
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00667
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00664
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00669
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00665
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00668
;  PRIOR FILING DATE: 2001-01-30
;  PRIOR APPLICATION NUMBER: PCT/US01/00663
;  PRIOR FILING DATE: 2001-01-30
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 15755
;  SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 7588
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-866-108A-7588

  Query Match             1.4%;  Score 13.8;  DB 1;  Length 17;
  Best Local Similarity   88.2%;  Pred. No. 1.1e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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RESULT 104
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; Sequence 7707, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
;  APPLICANT: GU, Yizhong
;  APPLICANT:  JI, Yonggang
;  APPLICANT:  PENN, Sharron G.
;  APPLICANT:  HANZEL, David K.
```

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
4.283 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 694 seqs, 13245 residues

Total number of hits satisfying chosen parameters: 1388

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 694 summaries

Database : rnpbdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	8	20	2.1	20	1	US-09-915-814-23	Sequence 23, Appl
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c	12	20	2.1	20	1	US-09-915-814-27	Sequence 27, Appl
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	97	15.4	1.6	22	1	US-10-114-270-417	Sequence 417, App
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108	15.2	1.6	20	1	US-10-317-803-209	Sequence 209, App
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c 137	14.8	1.5	20	1	US-09-863-806-44	Sequence 44, Appl
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c 181	14.4	1.5	17	1	US-10-723-361-7706	Sequence 7706, Ap
c 182	14.4	1.5	18	1	US-09-969-373-2805	Sequence 2805, Ap
183	14.4	1.5	18	1	US-10-606-133-215	Sequence 215, App
184	14.4	1.5	20	1	US-09-796-599-3	Sequence 3, Appli
c 185	14.4	1.5	20	1	US-09-957-837A-12	Sequence 12, Appl
c 186	14.4	1.5	20	1	US-09-828-344-146	Sequence 146, App
c 187	14.4	1.5	20	1	US-09-811-007-19	Sequence 19, Appl
c 188	14.4	1.5	20	1	US-10-062-624-19	Sequence 19, Appl
c 189	14.4	1.5	20	1	US-10-062-051-19	Sequence 19, Appl
c 190	14.4	1.5	20	1	US-10-062-920-19	Sequence 19, Appl
191	14.4	1.5	20	1	US-10-010-002-41	Sequence 41, Appl
192	14.4	1.5	20	1	US-10-309-814-3	Sequence 3, Appli
193	14.4	1.5	20	1	US-10-241-780-354	Sequence 354, App
194	14.4	1.5	20	1	US-10-241-780-355	Sequence 355, App
195	14.4	1.5	20	1	US-10-241-780-368	Sequence 368, App
196	14.4	1.5	20	1	US-10-241-780-369	Sequence 369, App
c 197	14.4	1.5	20	1	US-10-448-836-72	Sequence 72, Appl
198	14.4	1.5	20	1	US-10-160-807-168	Sequence 168, App
c 199	14.4	1.5	20	1	US-10-159-856-70	Sequence 70, Appl
200	14.4	1.5	20	1	US-10-159-856-124	Sequence 124, App
c 201	14.4	1.5	20	1	US-10-448-914A-72	Sequence 72, Appl
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203	14.4	1.5	20	1	US-10-185-057-23	Sequence 23, Appl
c 204	14.4	1.5	20	1	US-10-188-470-21	Sequence 21, Appl
c 205	14.4	1.5	20	1	US-10-289-762-6083	Sequence 6083, Ap
206	14.4	1.5	20	1	US-10-655-847-168	Sequence 168, App
207	14.4	1.5	20	1	US-10-304-116-47	Sequence 47, Appl
208	14.4	1.5	20	1	US-10-744-831-41	Sequence 41, Appl
c 209	14.4	1.5	20	1	US-10-680-349-19	Sequence 19, Appl
c 210	14.4	1.5	20	1	US-10-731-554-19	Sequence 19, Appl
211	14.4	1.5	20	1	US-10-915-856-15	Sequence 15, Appl
212	14.4	1.5	20	1	US-10-915-856-23	Sequence 23, Appl
213	14.4	1.5	20	1	US-10-492-928A-64	Sequence 64, Appl
c 214	14.4	1.5	20	1	US-10-954-723A-12	Sequence 12, Appl
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216	14.2	1.5	19	1	US-10-225-023-281	Sequence 281, App
c 217	14.2	1.5	19	1	US-10-225-023-1019	Sequence 1019, Ap
c 218	14.2	1.5	19	1	US-10-205-309-18	Sequence 18, Appl
219	14.2	1.5	19	1	US-10-205-309-343	Sequence 343, App
220	14.2	1.5	19	1	US-10-349-143-4520	Sequence 4520, Ap
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230	14.2	1.5	20	1	US-09-978-564A-21	Sequence 21, Appl
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c 232	14.2	1.5	20	1	US-09-784-674-487	Sequence 487, App
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247	14.2	1.5	20	1	US-09-978-298A-21	Sequence 21, Appl
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250	14.2	1.5	20	1	US-09-978-194A-21	Sequence 21, Appl
251	14.2	1.5	20	1	US-09-999-829A-21	Sequence 21, Appl
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 13, 2004, 08:26:32 ; Search time 11 Seconds
(without alignments)
3.553 Million cell updates/sec

Title: US-09-915-814-3
Perfect score: 2633
Sequence: 1 gacactaccaggatacagcc.....cctcccttgcaggtcggttt 2633

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 408 seqs, 7422 residues

Total number of hits satisfying chosen parameters: 816

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 408 summaries

Database : rnpb3.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	21	0.8	21	1	US-09-915-814-6	Sequence 6, Appli
3	20.6	0.8	21	1	US-09-765-081-171	Sequence 171, App
4	20.6	0.8	21	1	US-09-765-081-172	Sequence 172, App
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c 6	20	0.8	20	1	US-09-915-814-35	Sequence 35, Appl
c 7	20	0.8	20	1	US-09-915-814-36	Sequence 36, Appl
c 8	20	0.8	20	1	US-09-915-814-37	Sequence 37, Appl
c 9	20	0.8	20	1	US-09-915-814-38	Sequence 38, Appl
c 10	20	0.8	20	1	US-09-915-814-39	Sequence 39, Appl
c 11	20	0.8	20	1	US-09-915-814-40	Sequence 40, Appl
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c 124	20	0.8	20	1	US-09-915-814-175	Sequence 175, App
c 125	20	0.8	20	1	US-09-915-814-179	Sequence 179, App
c 126	20	0.8	20	1	US-09-915-814-183	Sequence 183, App
c 127	20	0.8	20	1	US-09-915-814-184	Sequence 184, App
c 128	20	0.8	20	1	US-09-915-814-185	Sequence 185, App
c 129	20	0.8	20	1	US-09-915-814-186	Sequence 186, App
c 130	20	0.8	20	1	US-09-915-814-192	Sequence 192, App
c 131	20	0.8	20	1	US-09-915-814-198	Sequence 198, App
c 132	20	0.8	20	1	US-09-915-814-203	Sequence 203, App
c 133	20	0.8	20	1	US-09-915-814-204	Sequence 204, App
c 134	20	0.8	20	1	US-09-915-814-212	Sequence 212, App
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c 136	19	0.7	20	1	US-09-915-814-221	Sequence 221, App
c 137	18.4	0.7	20	1	US-09-915-814-176	Sequence 176, App
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c 139	18.4	0.7	20	1	US-09-915-814-195	Sequence 195, App
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c 141	18.4	0.7	20	1	US-09-915-814-223	Sequence 223, App
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146	16.8	0.6	20	1	US-09-563-728A-7	Sequence 7, Appli
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c 149	16.8	0.6	20	1	US-09-915-814-168	Sequence 168, App
c 150	16.8	0.6	20	1	US-09-915-814-171	Sequence 171, App
c 151	16.8	0.6	20	1	US-09-915-814-181	Sequence 181, App
c 152	16.8	0.6	20	1	US-09-915-814-182	Sequence 182, App
c 153	16.8	0.6	20	1	US-09-915-814-188	Sequence 188, App
c 154	16.8	0.6	20	1	US-09-915-814-197	Sequence 197, App
c 155	16.8	0.6	20	1	US-09-915-814-202	Sequence 202, App
c 156	16.8	0.6	20	1	US-09-915-814-214	Sequence 214, App
c 157	16.8	0.6	20	1	US-09-915-814-222	Sequence 222, App
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c 163	16.4	0.6	20	1	US-10-371-474-63	Sequence 63, Appl
c 164	16.4	0.6	20	1	US-10-315-962-67	Sequence 67, Appl
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166	16	0.6	17	1	US-09-866-108-555	Sequence 555, App
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168	16	0.6	17	1	US-10-723-361-555	Sequence 555, App
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174	15.4	0.6	17	1	US-09-848-754A-3090	Sequence 3090, Ap
175	15.4	0.6	17	1	US-09-740-332-1617	Sequence 1617, Ap
176	15.4	0.6	17	1	US-09-817-879-1617	Sequence 1617, Ap
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178	15.4	0.6	17	1	US-10-238-700-2817	Sequence 2817, Ap
179	15.4	0.6	17	1	US-10-061-201-1478	Sequence 1478, Ap
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181	15.4	0.6	17	1	US-10-669-841-4210	Sequence 4210, Ap
182	15.4	0.6	17	1	US-10-723-361-556	Sequence 556, App
183	15.4	0.6	17	1	US-10-723-361-557	Sequence 557, App
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185	15.4	0.6	19	1	US-10-441-925A-22	Sequence 22, Appl
186	15.4	0.6	19	1	US-10-441-925A-24	Sequence 24, Appl
187	15	0.6	17	1	US-09-866-108-553	Sequence 553, App
188	15	0.6	17	1	US-09-866-108-1531	Sequence 1531, Ap
189	15	0.6	17	1	US-09-866-108-1532	Sequence 1532, Ap
190	15	0.6	17	1	US-09-866-108-1533	Sequence 1533, Ap
c 191	15	0.6	17	1	US-09-818-875-3582	Sequence 3582, Ap
192	15	0.6	17	1	US-09-818-875-3583	Sequence 3583, Ap
193	15	0.6	17	1	US-10-061-201-1479	Sequence 1479, Ap
194	15	0.6	17	1	US-10-061-201-1480	Sequence 1480, Ap
c 195	15	0.6	17	1	US-10-209-787-3582	Sequence 3582, Ap
196	15	0.6	17	1	US-10-209-787-3583	Sequence 3583, Ap
c 197	15	0.6	17	1	US-10-261-185-3582	Sequence 3582, Ap
198	15	0.6	17	1	US-10-261-185-3583	Sequence 3583, Ap
199	15	0.6	17	1	US-10-723-361-553	Sequence 553, App
200	15	0.6	17	1	US-10-723-361-1531	Sequence 1531, Ap
201	15	0.6	17	1	US-10-723-361-1532	Sequence 1532, Ap
202	15	0.6	17	1	US-10-723-361-1533	Sequence 1533, Ap
c 203	15	0.6	17	1	US-10-681-074-3582	Sequence 3582, Ap
204	15	0.6	17	1	US-10-681-074-3583	Sequence 3583, Ap
c 205	14.8	0.6	18	1	US-09-420-433-50	Sequence 50, Appl
c 206	14.8	0.6	18	1	US-09-961-077-1169	Sequence 1169, Ap
207	14.8	0.6	18	1	US-10-398-308-130	Sequence 130, App
208	14.8	0.6	18	1	US-10-227-719D-9	Sequence 9, Appli
209	14.8	0.6	18	1	US-10-283-881-17	Sequence 17, Appl
210	14.8	0.6	18	1	US-10-295-903-5	Sequence 5, Appli
c 211	14.8	0.6	18	1	US-10-178-325-161	Sequence 161, App
212	14.4	0.5	16	1	US-09-941-314-19	Sequence 19, Appl
213	14.4	0.5	16	1	US-09-829-155C-9	Sequence 9, Appli
214	14.4	0.5	16	1	US-09-943-388-15	Sequence 15, Appl
215	14.4	0.5	16	1	US-09-975-365-21	Sequence 21, Appl
c 216	14.4	0.5	16	1	US-10-712-672-1490	Sequence 1490, Ap
217	14.4	0.5	17	1	US-09-866-108-558	Sequence 558, App
c 218	14.4	0.5	17	1	US-09-866-108-2629	Sequence 2629, Ap
c 219	14.4	0.5	17	1	US-09-866-108-2630	Sequence 2630, Ap
220	14.4	0.5	17	1	US-09-866-108-2672	Sequence 2672, Ap
221	14.4	0.5	17	1	US-09-866-108-2673	Sequence 2673, Ap
c 222	14.4	0.5	17	1	US-09-877-478-117	Sequence 117, App
c 223	14.4	0.5	17	1	US-09-877-478-806	Sequence 806, App
224	14.4	0.5	17	1	US-09-848-754A-1396	Sequence 1396, Ap
225	14.4	0.5	17	1	US-09-848-754A-3089	Sequence 3089, Ap
226	14.4	0.5	17	1	US-09-848-754A-3091	Sequence 3091, Ap
227	14.4	0.5	17	1	US-09-740-332-1214	Sequence 1214, Ap
c 228	14.4	0.5	17	1	US-09-740-332-2938	Sequence 2938, Ap
c 229	14.4	0.5	17	1	US-09-740-332-2939	Sequence 2939, Ap
230	14.4	0.5	17	1	US-09-792-818-367	Sequence 367, App
c 231	14.4	0.5	17	1	US-09-855-612-7	Sequence 7, Appli
232	14.4	0.5	17	1	US-09-817-879-1214	Sequence 1214, Ap
c 233	14.4	0.5	17	1	US-09-817-879-2938	Sequence 2938, Ap
c 234	14.4	0.5	17	1	US-09-817-879-2939	Sequence 2939, Ap
235	14.4	0.5	17	1	US-10-297-134B-1	Sequence 1, Appli
c 236	14.4	0.5	17	1	US-10-342-902-117	Sequence 117, App
c 237	14.4	0.5	17	1	US-10-342-902-806	Sequence 806, App
c 238	14.4	0.5	17	1	US-09-927-046-1165	Sequence 1165, Ap
c 239	14.4	0.5	17	1	US-09-927-046-2170	Sequence 2170, Ap
c 240	14.4	0.5	17	1	US-10-156-306-5857	Sequence 5857, Ap
241	14.4	0.5	17	1	US-10-156-306-5980	Sequence 5980, Ap
c 242	14.4	0.5	17	1	US-10-238-700-2996	Sequence 2996, Ap
c 243	14.4	0.5	17	1	US-10-238-700-3518	Sequence 3518, Ap
244	14.4	0.5	17	1	US-10-061-201-1477	Sequence 1477, Ap
245	14.4	0.5	17	1	US-10-339-793-263	Sequence 263, App
c 246	14.4	0.5	17	1	US-10-712-672-452	Sequence 452, App
c 247	14.4	0.5	17	1	US-10-669-841-117	Sequence 117, App
c 248	14.4	0.5	17	1	US-10-669-841-806	Sequence 806, App
249	14.4	0.5	17	1	US-10-669-841-3807	Sequence 3807, Ap
c 250	14.4	0.5	17	1	US-10-669-841-5531	Sequence 5531, Ap
c 251	14.4	0.5	17	1	US-10-669-841-5532	Sequence 5532, Ap
252	14.4	0.5	17	1	US-10-723-361-558	Sequence 558, App

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: June 27, 2005, 16:51:28 ; Search time 0.001 Seconds
(without alignments)
296.820 Million cell updates/sec

Title: us-09-915-814-3
Perfect score: 970
Sequence: 1 cttcttgtaagagagtgcta.....tttctgagtgggtcgcagat 970

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 10 seqs, 153 residues

Total number of hits satisfying chosen parameters: 20

Minimum DB seq length: 8
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 10 summaries

Database : rstdb:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15.2	1.6	21	1	TA181D04Q	ACCESSION:AL474441
c	2	13.8	1.4	19	1	CL680274	ACCESSION:CL680274
c	3	12	1.2	12	1	CL436297	ACCESSION:CL436297
c	4	11.4	1.2	14	1	CL688513	ACCESSION:CL688513
c	5	11.4	1.2	16	1	BG897738	ACCESSION:BG897738
c	6	11.2	1.2	16	1	AJ594105	ACCESSION:AJ594105
	7	10.8	1.1	14	1	AJ688262	ACCESSION:AJ688262
c	8	10.8	1.1	15	1	CL439508	ACCESSION:CL439508
	9	10.4	1.1	13	1	BQ586028	ACCESSION:BQ586028
	10	10.4	1.1	13	1	CL437480	ACCESSION:CL437480

ALIGNMENTS

RESULT 1
TA181D04Q/c
LOCUS TA181D04Q 21 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 181d04, reverse sequence, genomic survey sequence.
ACCESSION AL474441
VERSION AL474441.1 GI:11839655
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .21
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="181d04"

Query Match 1.6%; Score 15.2; DB 1; Length 21;
Best Local Similarity 85.0%; Pred. No. 0.59;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        823 ACAGTCAGACAAGCAAACAA 842
              |||| || |||| |||||||
Db         21 ACAGACAAACAAACAAACAA 2
```

RESULT 2
CL680274/c
LOCUS CL680274 19 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0128c_E09_2 - PRI0128c.BR (19) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL680274
VERSION CL680274.1 GI:50187117
KEYWORDS GSS.
SOURCE Pristionchus pacificus
ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
source 1. .19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"

Query Match 1.4%; Score 13.8; DB 1; Length 19;
Best Local Similarity 88.2%; Pred. No. 1.1;

```
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        164 AAGAGGAAGTGCCATCA 180
              ||| ||||||| |||||
Db         17 AAGGGGAAGTGTCATCA 1


RESULT 3
CL436297/c
LOCUS       CL436297                  12 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST2689-NL.Seq MICB1 Mus musculus genomic clone PST2689-NL.Seq,
            genomic survey sequence.
ACCESSION   CL436297
VERSION     CL436297.1  GI:45570957
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 12)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST2689-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST2689-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"

  Query Match             1.2%;  Score 12;  DB 1;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2.5;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        468 CTGCACAACATG 479
              ||||||||||||
Db         12 CTGCACAACATG 1


RESULT 4
CL688513/c
LOCUS       CL688513                  14 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0149c_G04_2 - PRI0149c.BR (14) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL688513
VERSION     CL688513.1  GI:50197591
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"

  Query Match             1.2%;  Score 11.4;  DB 1;  Length 14;
  Best Local Similarity   92.3%;  Pred. No. 3.3;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        198 ATCTGTGAAGAGA 210
              ||| |||||||||
Db         14 ATCAGTGAAGAGA 2


RESULT 5
BG897738/c
LOCUS       BG897738                  16 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HOA17-1-C3 HOA (Human Osteoarthritic Cartilage) Homo sapiens cDNA,
            mRNA sequence.
ACCESSION   BG897738
VERSION     BG897738.1  GI:14307987
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
   PUBMED   11597177
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /clone_lib="HOA (Human Osteoarthritic Cartilage)"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
```

Directional"

Query Match 1.2%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 3.3;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy        116 AGCTGCCTTAAAA 128
              ||||||||||| |
Db         15 AGCTGCCTTAATA 3
```

RESULT 6
AJ594105/c
LOCUS AJ594105 16 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 392H06, genomic survey sequence.
ACCESSION AJ594105
VERSION AJ594105.1 GI:37943729
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 16)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .16
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="392H06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .16
/note="T-DNA flanking sequence
left border"

Query Match 1.2%; Score 11.2; DB 1; Length 16;
Best Local Similarity 81.2%; Pred. No. 3.6;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy        474 AACATGATGCTGAATC 489
              || || || |||||||
Db         16 AAAATTATACTGAATC 1
```

RESULT 7
AJ688262
LOCUS AJ688262 14 bp mRNA linear EST 29-JUN-2004
DEFINITION AJ688262 KN261 Bos taurus cDNA clone KN261-047_O17, mRNA sequence.
ACCESSION AJ688262
VERSION AJ688262.1 GI:49420852
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 14)
AUTHORS Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
TITLE Development of cDNA and EST resources for studying reproduction and embryo development in pigs and cattle
JOURNAL Unpublished (2004)
COMMENT Contact: Anderson SI
Genomics and Bioinformatics
Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred v0.020425.c. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options. Vector:pBlueScriptII(SK+) R. Site1: EcoRI R. Site2: SmaI 3' Seq Primer M13F Normalised library constructed from bovine ovary. Clones available from UK Centre for Functional Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES Location/Qualifiers
source 1. .14
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
/clone="KN261-047_O17"
/tissue_type="ovary"
/clone_lib="KN261"
/note="Vector: pBlueScriptII(SK+); Site_1: EcoRI; Site_2: SmaI; Single pass sequencing. Normalised library constructed from bovine ovary."

Query Match 1.1%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 4.3;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy        890 GGATTTCTAACAAA 903
              | |||||||| |||
Db          1 GAATTTCTAAAAAA 14
```

RESULT 8
CL439508/c
LOCUS CL439508 15 bp DNA linear GSS 18-MAR-2004
DEFINITION PST9427-NR.Seq MICB1 Mus musculus genomic clone PST9427-NR.Seq, genomic survey sequence.
ACCESSION CL439508
VERSION CL439508.1 GI:45577088
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 15)
AUTHORS Hicks,G.G.
TITLE www.EScells.ca
JOURNAL Unpublished (2002)
COMMENT Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, Universitry of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from

```
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST9427-NR.Se
            q
            Class: Gene Trap.
FEATURES              Location/Qualifiers
     source           1. .15
                      /organism="Mus musculus"
                      /mol_type="genomic DNA"
                      /strain="129 sv"
                      /db_xref="taxon:10090"
                      /clone="PST9427-NR.Seq"
                      /sex="Male"
                      /cell_type="Embryonic stem cell"
                      /cell_line="D3H (J1 subclone)"
                      /clone_lib="MICB1"
                      /note="Vector: U3NeoSV1"

  Query Match             1.1%;  Score 10.8;  DB 1;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 4.3;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy        480 ATGCTGAATCCCAG 493
              ||||||| | ||||
Db         14 ATGCTGAGTTCCAG 1


RESULT 9
BQ586028
LOCUS       BQ586028                 13 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012394-024-013-F21-SP6 MPIZ-ADIS-024-leaf Beta vulgaris cDNA clone
            024-013-F21 5-PRIME, mRNA sequence.
ACCESSION   BQ586028
VERSION     BQ586028.1  GI:26115610
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 13   Std Error: 0.00
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                      cDNA library from sugar beet, library provided by KWS
                      Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                      b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                      orientation:
                      SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                      Sequencing granted in the context of the GABI-Beet
                      project, local PI: Dr. Katharina Schneider, coordinator:
                      Prof. Christian Jung;  Sequence submission managed by
                      RZPD/GABI-Primary database:http://gabi.rzpd.de"

  Query Match             1.1%;  Score 10.4;  DB 1;  Length 13;
  Best Local Similarity   91.7%;  Pred. No. 5.1;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        518 TCTGCTTCACAA 529
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Db          2 TCTGCTTAACAA 13


RESULT 10
CL437480
LOCUS       CL437480                 13 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST5604-NR.Seq MICB1 Mus musculus genomic clone PST5604-NR.Seq
            similar to BC031407, genomic survey sequence.
ACCESSION   CL437480
VERSION     CL437480.1  GI:45573210
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
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            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST5604-NR.Se
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Qy        907 TCAGGAACTATC 918
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Db          1 TCAGGAAGTATC 12


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